

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2005, 10:53:33 ; Search time 5243 Seconds
(without alignments)

4239.850 Million cell updates/sec

Title: US-10-828-332-7

Perfect score: 3107

Sequence: 1 MGVSSSLPTMTSGDRYP.....LETPALATKYVTVYTNHAI 584

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 13032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cpn2.1/USPTO.spool/US10828332/runat.17062005.170038.7263/app.query.fasta_1.775
-DB=EST -QFMT=fstap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2348	75.6	3675	AK038395	AK038395 Mus muscu
2	2348	75.6	3693	BC051384	BC051384 Mus muscu
3	2298	74.0	2671	AY406143	AY406143 Homo sapi
4	2280.5	73.4	2667	AY406145	AY406145 Mus muscu
5	2229.5	71.8	2671	AY406144	AY406144 Pan trogl
6	2219	71.4	2748	AY401208	AY401208 Homo sapi
7	2214	71.3	2748	AY401210	AY401210 Mus muscu
8	2156.5	69.4	4209	AK053447	AK053447 Mus muscu
9	2140	68.9	2611	AY401209	AY401209 Pan trogl

10	2025	65.2	3399	3	BC034118	BC034118 Mus muscu
11	1298.5	41.8	1484	3	CR717163	CR717163 Tetraodon
12	1294	41.6	782	6	CD353576	CD353576 UI-M-GMO-
13	1169	37.6	1051	9	CNS041PP	AL306790 Tetraodon
14	1151	37.0	711	7	CN409312	CN409312 170004243
15	1114.5	35.9	3879	3	AK032422	AK032422 Mus muscu
16	1066	34.3	853	1	AU296039	AU296039 AU296039
17	1034.5	33.3	973	4	B1827857	B1827857 603074065
18	1023	32.9	795	7	CN460548	CN460548 UI-M-HBO-
19	1019	32.8	678	5	B0205182	B0205182 604156686
20	1013	32.6	702	7	CK134839	CK134839 SB0204082
21	983	31.6	787	4	B1732193	B1732193 603352796
22	964	31.0	582	5	BP359939	BP359939 BP359939
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24	943	30.4	679	5	BM964289	BM964289 UI-M-EQO-
25	928	29.9	732	6	CD609655	CD609655 56040124H
26	916.5	29.5	723	6	CA344834	CA344834 675311 NC
27	915.5	29.5	839	9	CNS028BY	AL185767 Tetraodon
28	885.5	28.5	1101	9	CNS04XAU	AL311439 Tetraodon
29	884.5	28.5	2182	3	AK034263	AK034263 Mus muscu
30	872.5	28.1	772	5	BX873944	BX873944 BX873944
31	860	27.7	666	9	CE724887	CE724887 tigr-g88-
32	821.5	26.4	645	6	CD280064	CD280064 G44469.19
33	817.5	26.3	895	4	BG261524	BG261524 602373277
34	800.5	25.8	665	6	CA408051	CA408051 STR00549
35	799	25.7	777	5	B0456417	B0456417 603217533
36	770.5	24.8	633	6	CB517356	CB517356 sealrbs3
37	766.5	24.7	1029	3	CNS02AUZ	AL189044 Tetraodon
38	763.5	24.6	1736	3	AK002958	AK002958 Mus muscu
39	758	24.4	1078	9	CNS054KQ	AL320867 Tetraodon
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41	744.5	24.0	941	2	BE779818	BE779818 601465317
42	735.5	23.7	872	9	CNS02JYJ	AL200851 Tetraodon
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44	723	23.3	562	6	CD252943	CD252943 AGENCOURT
45	721	23.2	521	7	CN468842	CN468842 hh_Ab_Bra

ALIGNMENTS

RESULT 1

AK038395

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

AK038395 3675 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male hypothalamus cDNA, RIKEN full-length
enriched library, clone:A23002004 product:METABOTROPIC GLUTAMATE
RECEPTOR 8 PRECURSOR, full insert sequence.

AK038395

AK038395.1 GI:26086504

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Muridae; Sciurognathi; Muridae; Mus.

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
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ORIGIN

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Pred. No.: 1,798-225 Length: 2671
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 Best Local Similarity: 75.44% Mismatches: 83
 Query Match: 73.96% Indels: 4
 DB: 9 Gaps: 3

US-10-828-332-7 (1-584) x AY406145 (1-2671)

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 QY 22 SerArgThrLeuAspAsnAsnArgArgAsnIleTyrPheAlaGluPheTrpGluAspAsn 41
 DB 1039 ACCCGAAGCTTGTGCCAATAATCGAAGAAATGTGTTTGCAGAAATTTCTGGGAGGAGAT 1098
 QY 42 PheHisCysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
 DB 1099 -TTTGGCTGCAAGTTAGGATCATCATGGG---AAAAGCAACAGTCATATAAGAAATGCACA 1155
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 QY 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
 DB 1216 ATTGATGCTGTATATTCATGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 1275
 QY 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr 121
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 DB 1570 AAGAAAACGGTGAAGGGGCTCTTGTCTGCTGGCACTGTGAACGCTGTGAAGTTACAAAC 1629
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RESULT 4
 AY406145
 LOCUS

AY406145 2667 bp DNA linear GSS 15-DEC-2003

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 QY 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
 DB 1750 GTGCTGTGTGTGTGCAATATTTGGAATCATCGCCACCCACCTTTGTGATCGTACCTTT 1809
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 DB 1870 CTAAACGGGGATTTTCTCTGTATTCAATCAGTTTAAATGATTCGACACCATACATA 1929
 QY 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
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 QY 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyArgSerValSer 361
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 QY 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
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 QY 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
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DEFINITION Mus musculus GRM8 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406145
VERSION AY406145.1 GI:39762119
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Alignment Scores:
Pred. No.: 1,15e-223 Length: 2667
Score: 2280.50 Matches: 427
Percent Similarity: 84.81% Conservative: 53
Best Local Similarity: 75.44% Mismatches: 81
Query Match: 73.40% Indels: 6
Dbs: 9 Gaps: 4

US-10-828-332-7 (1-584) x AY406145 (1-2667)
QY 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 979 GGAGCTGTGCACAAATTTGCCCAAGAGACATCAATGTATGGTTGACCGTACTTTAGA 1038
QY 22 SerArgThrLeuAspAsnArgAsnArgAsnLeuPheAlaGluPheTyrGluAspAsn 41
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QY 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
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1690 CGCACTGGCTGCCAGAGGATTCATCATCAAGTTGGAGTGGCATTCACCTGGGCGGTG 1749
262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
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 Db 2434 GCTCAATCAGCGGAAAGCTCTACATACAACTACACAGCTTACACCTTCCATGAACCTA 2493
 QY 501 SerAlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuLeuPheHis 520
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 LOCUS AY401210
 DEFINITION Mus musculus GRM7 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY401210
 VERSION AY401210.1 GI:39757199
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2748)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 2748)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
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 Best Local Similarity: 71.26% Indels: 2
 Query Match: 9 Gaps: 2
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/

FEATURES

Location/Qualifiers

source

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ORIGIN

Alignment Scores:

Pred. No.:	1.53e-210	Length:	4209
Score:	2156.50	Matches:	400
Percent Similarity:	83.39%	Conservative:	72
Best Local Similarity:	70.67%	Mismatches:	92
Query Match:	69.41%	Indels:	3
DB:	3	Gaps:	2

US-10-828-332-7 (1-584) x AK053447 (1-4209)

QY	3	GlyValSerSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer	21
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QY	22	SerArgThrLeuAspAenAsnArgArgAenIleTTPheAlaGluPheTrpGluAspAen	41
DB	1376	TCCCGACACTTGAACCAACAGGAGAAATGATGTTGGCGATATCTGGAGAGAAC	1435
QY	42	PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr	61
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QY	62	AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal	81
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QY	102	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysValTyr	121
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QY	161	TyrLysValIleGlySerTrpThrAspHisLeuArgIleGluArgMetGlnTrp	180
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QY	201	ArgLysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyr	220
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QY	221	GlnTyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGlu	240
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QY	241	AsnArgThrSerCysGlnProIleValLysLeuGluTrpAspSerProTrpAla	260
DB	2034	RACCGAATGGCTGTGAGAACATCCCATCATCAACTGGAGTGGCACTCCCTCCCTGGCT	2093
QY	261	ValLeuProLeuPheLeuAlaValValGlyIleAlaIleThrLeuPheValValThr	280
DB	2094	GTAATTCCTGCTCTCTCGCAATGTTGGGATCATTCGCACCATCTTGTGTATGCAACC	2153
QY	281	PheValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTrpVal	300
DB	2154	TTCATCCCTCAATGATACACCCATCGTGGGCACTCGGCGGGAATCTAGCTATGTT	2213
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DB	2214	TTATTCAGGAGCATCTTCTCTGCTATATCATCATCTTCTTATGATTCGCAAGCAGAT	2273
QY	321	LeuGlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTrpAla	340
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QY	401	PheGlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIle	420
DB	2514	TACGATGAGCATATGACAACTGAACCCCAAGACCAAGACGAGGAGGTCTCAAAATGTG	2573
QY	421	SerAspLeuSerLeuIleCysLeuGlyTyrSerMetLeuLeuMetValThrCysThr	440
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Qy 461 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr 480
 Db 2694 TTCACTATGTACAGACTGTATCGTATGGCTTGCCTTCATCCCAATATTTTGGCACA 2753

Qy 481 SerGlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerIleu 500
 Db 2754 GCGCAATCAGCAGAAAGCTTACATACAAACCCACCGCTTACAACTCCATGAACCTA 2813

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Qy 521 ProGluGlnAenValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThr 540
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Qy 541 MetSerAenLysPheThrGlnLysGlyAsnPheArgProAenGlyGluAlaLysSerGlu 560
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Qy 561 LeuCysGluAenLeuGlu 566
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RESULT 9
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 LOCUS Pan troglodytes GRM7 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY401209
 VERSION AY401209.1 GI:39757198
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1 (bases 1 to 2611)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 JOURNAL
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 Location/Qualifiers
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 Score: 2140.00 Matches: 396
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Best Local Similarity: 67.81% Mismatches: 114
 Query Match: 68.88% Indels: 2
 DB: 9 Gaps: 2

US-10-828-332-7 (1-594) x AY401209 (1-2611)

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Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr 121
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Qy 122 IleArgAsnValAenPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
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Qy 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySer---AlaGlu 160
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Qy 161 TyrLysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrp 180
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RESULT 10

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 LOCUS
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 ACCESSION BC034118
 VERSION BC034118.1 GI:21706621
 KEYWORDS HTC.
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3399)
 REFERENCES
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shcherchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalka, U., Smalil, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932
 2 (bases 1 to 3399)
 Strausberg, R.
 Direct Submission
 Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 44 Row: i Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis

This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers
 1. 3399
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 /clone="IMAGE:4511841"
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 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

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 Score: 2025.00 Matches: 371
 Percent Similarity: 80.04% Conservative: 62
 Best Local Similarity: 68.58% Mismatches: 104
 Query Match: 65.18% Indels: 4
 DB: 3 Gaps: 2

US-10-828-332-7 (1-584) x BC034118 (1-3399)

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 Db 122 GGGCCATCACCATCTTTCGCAAAAGGGCTTCAATCGACGGATTTGACCACTATTATG 181
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 Qy 22 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
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 Db 182 ACTGCTCCCTGGAGAACACCGCAGAAACATCTGTTGCTGTGAGATCTCTGGAGAGAGAT 241
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Qy      213  HisCysGluProCysThrGlyThrGlnValAspArgTyrThrCysLysThrCys 232
Db      198  CACTGTGAGCGCTGCATGGCTATCAATACAGCGCTGACACCTPACACATGCAAGATGTGT 257
Qy      233  ProTyrAspMetArgProThrGluAsnArgThrSerCysGlnProIleProIleValLys 252
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Qy      253  LeuGluTrpAspSerProTrpAlaValLeuProLeuPheLeuAlaValValGlyIleAla 272
Db      318  TTAGAGTGGAGCTCTCCATGGCGCAGTCATCCCTGTGCTAATTGCAGTCATCGGTATCATG 377
Qy      273  AlaThrLeuPheValValThrPheValArgTyrAsnAspThrProIleValLysAla 292
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Qy      293  SerGlyArgGluLeuSerTyrValLeuAlaGlyIlePheLeuCysTyrAlaThrThr 312
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Qy      313  PheLeuMetIleAlaGluProAspLeuGlyThrCysSerLeuArgArgIlePheLeuGly 332
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Qy      333  LeuGlyMetSerIleSerTyrAlaAlaLeuLeuThrLysThrAsnArgIleTyrArgIle 352
Db      558  CTGGGATGAGCATCATGTTACGCTGCTTGTACCAAAACCAATCGCATTTACCGTATT 617
Qy      353  PheGluGlnGlySerValSerAlaProArgPheIleSerProAlaSerGlnLeu 372
Db      618  TTGTACAGGACCATCATGCTGTCAACGGCGCCCAAGTTCTTCTCCAGCATCTCAACTG 677
Qy      373  AlaIleThrPheIleLeuIleSerLeuGlnLeuLeuGlyIleCysValTrpPheValVal 392
Db      678  GTCATCACCTTCAGCTTGCCCTCAGTCAGCTGCTGTGTGTATGATCTGTTATCGCC 737
Qy      393  AspProSerHisSerValValAspPheGlnAspGlnArgThrLeuAspProArgPheAla 412
Db      738  GATCCCTCCAAAGCAATTATTGACTACGAGGACGAGGACATCAAAACCCGACCATGGCT 797
Qy      413  ArgGlyValLeuLysCysAspIleSerAspLeuSerLeuIleCysLeuLeuGlyTyrSer 432
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Qy      433  MetLeuLeuMetValThrCysThrValTyrAlaIleLysThrArgGlyValProGluThr 452
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Qy      453  PheAsnGluAlaLysPheProIleGlyPheThrMetTyrThrThr--CysIleValTrpLeu 472
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Qy      472  IaPheIleProIlePhePheGlyThrSerGlnSerAlaAspLysLeuTyrIleGlnThrT 492
Db      978  CATGATCCCAATCTTATTGGCAGCTGCGCATGCTCCAGAAAAGGTAAACACACAA---- 1033
Qy      492  hrThrLeuThrValSerValSerLeuSerAlaSerValSerLeuGlyMetLeuTyrMetP 512
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Qy      512  roLysValTyrIleLeuPheHisProGluGln 523
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RESULT 12

CD353576

LOCUS

782 bp mRNA linear EST 15-JUL-2003

DEFINITION

UI-M-GM0-cgc-a-23-0-UI.r1 NIH_BMAP_GM0 Mus musculus cDNA clone
IMAGE:30360694 5', mRNA sequence.

ACCESSION

CD353576

VERSION

CD353576.1 GI:31146077

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

REFERENCE

1 (bases 1 to 782)

AUTHORS

Contact: Robert Strausberg, Ph.D.

TITLE

Email: cgbbs-remail.nih.gov

JOURNAL

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

COMMENT

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES

Seq primer: pYX-5

source

Location/Qualifiers

1..782

/organism="Mus musculus"

/mol_type="mRNA"

/strains="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30360694"

/tissue_type="whole brain"

/dev_stage="1, 5 and 15 days newborn"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP GM0"

/note="Organ: Brain; Vector: pYX-Asc; Site: 1; Ecor I;

Site 2: Not I; The library was constructed according

Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was size
selected according to mRNA size fraction, ligated with Ecor
I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 1,268-122 Length: 782

Score: 1294.00 Matches: 256

Percent Similarity: 98.85% Conservative: 1

Best Local Similarity: 98.46% Mismatches: 3

Query Match: 41.65% Indels: 0

DB: 6 Gaps: 0

US-10-828-332-7 (1-584) x CD353576 (1-782)

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Db 1 CCCTGGGCTGTGCTGCCCTCTTCTGCTGTGGGCAATGCTGCCACCGCTGTCTGTG 60

Qy 278 ValValThrPheValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeu 297

Db 61 GTGGTCACTTTTGTGGCTACACGACACTCCGATCGTCAAGGCCCTCGGCGGAGCTG 120

Qy 298 SerTyrValLeuLeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAla 317

Db 121 AGCTACGCTGCTGGCGGCGCATCTTCTCTGCTATGCCACACCTTCTCATGATCGCA 180

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Qy 318 GluProAspLeuGlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIle 337
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Qy 338 SerTyrAlaAlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLys 357
Db 241 AGCTACGGCGCCCTGCTGACCAAGACCAACCGCATCTACCGCATCTTTTGACAGGGCAAG 300
Qy 358 ArgSerValSerAlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIle 377
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Qy 378 LeuIleSerLeuGlnLeuLeuGlyIleCysValTyrPheValValAspProSerHisSer 397
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Qy 398 ValValAspPheGlnAspGlnArgThrLeuAspProArgPheAlaAtgGlyValLeuLys 417
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Qy 418 CysAspIleSerAspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetVal 437
Db 481 TGTGACATCTCGGACCTGCTCATCTGCTCTCTCTGGGCTACAGCATGCTGCTGATGTC 540
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Qy 458 ProIleGlyPheThrMetTyrThrThrCysIleValTyrPheLeuAlaPheIleProIlePhe 477
Db 601 CCCATCGGCTTCCACATGATACACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy 478 PheGlyThrSerGlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSer 497
Db 661 TTTGGCAGCTCGCAGTCGGCTGACAAAGCTGTACATCCAGACACCACTGACGGTCTCT 720
Qy 498 ValSerLeuSerAlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIle 517
Db 721 GTGAGTCTGAGCGCTTCAAGTTCCTGGGGATGCTTACATGCCCCANNAGTCTACATCATC 780

CNS04TPP 1051 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence SP6 end of clone
034012 of library B from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL306790
VERSION AL306790.1 GI:8207596
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernet,A., Fitzames,C., Wincker,P., Brottier,P., Quetier,P.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fitzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,P.,
Saurin,W., Bernet,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
```

```
10899143
PUBMED 3 (bases 1 to 1051)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
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Qy 212 TrrHisCysGluProCysThrGlyTyrGlnValAspArgTyrThrCysLysThr 231
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Db 967 TGGCGCTATGATTGGCGCCAAATGGGAATCACACTGGCTGTGANCCTATCCCCANTGTT 908
Qy 252 LysLeuGlnTrrAspSerProTrrAlaValLeuProLeuPheLeuAlaValValIle 271
Db 907 AAGCTGGAGTGGAGCTCNCATGGGCANTCATCCCTGTTCTCATCGCTGCTCGGAATC 848
Qy 272 AlaAlaThrLeuPheValValValThrPheValArgTyrAsnAspThrProIleValLys 291
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Qy 292 AlaSerGlyArgGluLeuSerTyrValLeuLeuAlaGlyIlePheLeuCysTyrAlaThr 311
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Qy 312 ThrPheLeuMetIleAlaGluProAspLeuGlyThrCysSerLeuArgArgIlePheLeu 331
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Qy 372 LeuAlaIleThrPheIleLeuIleSerLeuGlnLeuLeuGlyIleCysValTrrPheVal 391
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Qy 392 ValAspProSerHisSerValValAspPheGlnAspGlnArgThrLeuAspProArgPhe 411
Db 487 GTTACCCGCTCAAGCCATCATCATGTAGAGACCAAGCCAGCAGCATTAATCCGAAATG 428
Qy 412 AlaArgGlyValLeuLysCysAspIleSerAspLeuSerLeuIleCysLeuLeuGlyTyr 431
```


Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multiplexed sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3879)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 Location/Qualifiers
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 putative"
 misc_feature
 ORIGIN
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 Score: 1114.50 Matches: 234
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 Query Match: 35.87% Indels: 39
 DB: 3 Gaps: 10
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 Db 573 CTCGGCCAGAAACAAACCTCAGAAACCTTGGTTTCAAGAAATTTTGGCAGCATCGTTT 632
 Qy 43 HisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisLysLysCysThrAsn 62
 Db 633 CAGTCCGGCTAGAGGGTTTGCAAGAGCAAGCAAGTACACAAAGAGCTGCAACAGT 692
 Qy 63 ArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheValIle 82
 Db 693 -----TCTCTAAGTCTGAGAACGCATCTGTTCAAGATTCCAAAATTTGGGATTTGTATC 746
 Qy 83 AspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysProGly 102
 Db 747 AATGCAATCTATTATATGCTTATGGCTCCACAAATGCAGATGTCCCTGTGTCCAGGC 806
 Qy 103 ArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysLysIle 122
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 Qy 123 ArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGlyAsp 142
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 Qy 143 AlaProGlyArgTyrAspIleTyrGlnTyr---GlnLeuArgAsnGlySerAlaGluTyr 161
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 Qy 162 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
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 Qy 202 LysLysThrValLysGly---MetAlaCysCysTrpHisCysGluProCysThrGlyTyr 220
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 Db 1284 ATTGCAGCTGGGTGGTTGGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343
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QY 361 -----SerAlaProhghPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeu 378
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QY 379 IleSerLeuGlnLeuGlyIleCysValTrpPheValValAspProSerHisSerVal 398
Db 1644 ATCTGTATACAGTTGGGTATTATTGTGGCCCTCTTTATCATGGAGCCTCCGGATATAATG 1703
QY 399 ValAspPheGlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCys 418
Db 1704 CATGACTAT-----CCAAGCATCCGAGAGTCTACTTTGATTGT 1742
QY 419 AspileSerAspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThr 438
Db 1743 AACACCACCAACCTAGGGTGTCTCTCTTGGATACAATGGATTATTGATTTTGAGT 1802
QY 439 CysThrValTyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysPro 458
Db 1803 TGCATTTCTATGCGTTCAAGACCAGAAATGTTCCAGCCAACCTTTAACGAGGCCAAATAT 1862
QY 459 IleGlyPheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePhe 478
Db 1863 ATTGCTTTACCATGTACACACCTGCATCATATGGCTGGCCTTTGTGCTATCTACTTT 1922
QY 479 GlyThrSerGlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerVal 498
Db 1923 GGCAGCAAC-----TACAAAATCATCACCATGTGTCTCAGTC 1961
QY 499 SerLeuSerAlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeu 518
Db 1962 AGCCTCAGTGCCACAGTGGCCCTGGTTCATGTTGTGCCGAAGGTGACATCATCTCTA 2021
QY 519 PheHisProGluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAla 538
Db 2022 GCCAAACCGAGAGAAATGTG-----CGCAGCGCCTTCACAACC 2060
QY 539 AlaThrMetSerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLys 558
Db 2061 TCTACAGTGGTGGCATGCACGTA-----GGAGATGGCAAG 2096
QY 559 SerGluLeu---CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrVal 577
Db 2097 TCATC-ATCCGCTGCCAGATCCAGAGCCTAGTCAACCTGTGGAAGAGAGGGGCTC 2155
QY 578 ThrTyrThrAsn 581
Db 2156 GTCTGGGGNAAC 2167

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Job time : 5291 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2005, 11:28:54 ; Search time 280 Seconds
(without alignments)
3412.806 Million cell updates/sec

Title: US-10-828-332-7

Perfect score: 3107

Sequence: 1 MGVSSSLPTRMTSGDFRYF.....LETPALATKQTVYVYTNHAI 584

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFWT=fascap -SUFFIX=rni -MINMATCH=0.1 -LOOCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	98.2	2838	4	US-09-820-809-1
2	3050.5	98.2	4095	5	PCT-US91-09422-18
3	3004.5	95.7	2736	3	US-08-617-785-1
4	3004.5	96.7	2736	4	US-09-817-464-1
5	3004.5	96.7	3431	3	US-09-641-318-1
6	3004.5	96.7	3431	3	US-09-641-318-3
7	3004.5	96.7	3884	4	US-09-016-434-1074
8	3004.5	96.7	3884	4	US-09-820-809-14
9	2720.5	87.6	2426	5	PCT-US91-09422-20
10	2370	76.3	3321	3	US-08-855-146-1
11	2370	76.3	3321	3	US-08-855-146-3
12	2348	75.6	3833	3	US-08-823-110-2

13	2348	75.6	3833	3	US-08-604-298-2	Sequence 2, Appli
14	2328	74.9	2724	3	US-08-823-110-5	Sequence 5, Appli
15	2328	74.9	2724	3	US-08-604-298-5	Sequence 5, Appli
16	2219	71.4	2745	3	US-08-617-785-11	Sequence 11, Appl
17	2219	71.4	2745	4	US-09-817-464-11	Sequence 11, Appl
18	2219	71.4	3021	4	US-09-016-434-1118	Sequence 1118, Ap
19	2210	71.1	2997	1	US-08-453-862-1	Sequence 1, Appli
20	2210	71.1	2997	2	US-08-452-734A-1	Sequence 1, Appli
21	2210	71.1	2997	3	US-08-176-401B-1	Sequence 1, Appli
22	2210	71.1	2997	5	PCT-US94-14989-1	Sequence 1, Appli
23	2191.5	70.5	2766	3	US-08-617-785-13	Sequence 13, Appl
24	2191.5	70.5	2766	4	US-09-817-464-13	Sequence 13, Appl
25	2191.5	70.5	3804	3	US-08-617-785-3	Sequence 3, Appli
26	2191.5	70.5	3804	4	US-09-817-464-3	Sequence 3, Appli
27	2052.5	66.1	2961	2	US-08-407-875-1	Sequence 1, Appli
28	2052.5	66.1	2961	3	US-09-277-858-1	Sequence 1, Appli
29	2040.5	65.7	2670	3	US-09-126-280-1	Sequence 1, Appli
30	2022	65.1	2635	3	US-09-126-280-3	Sequence 3, Appli
31	1865.5	60.0	1588	3	US-08-617-785-7	Sequence 7, Appli
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35	1172.5	37.7	2619	3	US-09-258-523-1	Sequence 1, Appli
36	1172.5	37.7	2619	3	US-09-258-523-3	Sequence 3, Appli
37	1155.5	37.2	2637	3	US-08-794-158-1	Sequence 3, Appli
38	1155.5	37.2	2637	3	US-08-794-158-3	Sequence 3, Appli
39	1155.5	37.2	3410	4	US-09-016-434-1080	Sequence 1080, Ap
40	1150.5	37.0	2621	4	US-09-016-434-1490	Sequence 1490, Ap
41	1148.5	37.0	3919	1	US-08-072-574-5	Sequence 5, Appli
42	1148.5	37.0	3919	1	US-08-486-270-5	Sequence 5, Appli
43	1148.5	37.0	3919	3	US-08-367-284-5	Sequence 5, Appli
44	1148.5	37.0	3919	3	US-09-153-757-5	Sequence 5, Appli
45	1148.5	37.0	3919	4	US-09-459-715-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-820-809-1
; Sequence 1, Application US/09820809
; Patent No. 6608176
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; APPLICANT: ROOPER, STEPHEN D.
; TITLE OF INVENTION: TTASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820,809
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-820-809-1

Alignment Scores:		Length:	2838
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Score:	3050.50	Conservative:	2
Percent Similarity:	98.97%	Mismatches:	5
Best Local Similarity:	98.63%	Indels:	1
Query Match:	98.18%	Gaps:	1
DB:	4		

US-10-828-332-7 (1-584) x US-09-820-809-1 (1-2838)

Qy	3	GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer	21
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Qy	22	SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn	41

Db 252 AGCCGCGAGCTGGAGCAACACAGCGCAACATCTGTTTGGCGAGTTCTGGGAGCAAC 311
Qy 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
Db 312 TTCCATTGCAAGTTGAGCGCGCAGCGCTCAAGAGGGAAGGAGCCACATCAAGAAGTGACCC 371
Qy 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGlnGlnGluGlyLysValGlnPheVal 81
Db 372 AACCGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCAGGAGGGAAGGTGCAGTTCTGTG 431
Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 432 ATTGACGCTGTGTAGCGCATGGGCCACGCGCTGCACGCCATGCACCGTGACTGTGTCT 491
Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
Db 492 GCGCGGTAGGACTCTGCCCTCGCATGCGACCCCGTGGATGGCACCCAGCTGCTTAAGTAC 551
Qy 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
Db 552 ATCAGGAAGTCAACTTCTAGGCAATTGCGGGGAACCTGTAACTTCTCAATGAGNACGGA 611
Qy 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
Db 612 GACGCACCGGCGCTACGACATCTACCAGTACCACTGCGCAATGGCTCGGCCGAGTAC 671
Qy 162 LysValIleGlySerThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
Db 672 AAGGTATCGGCTCGTGACAGACACCTGTCACCTCAGAATAGAGCGGATGCACTGGCCA 731
Qy 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
Db 732 GGGAGTGCCAGAGCTGCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGGAGCGA 791
Qy 202 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
Db 792 AAGAAGACTGTGAAGGCGATGGCTTGTCTGGCTGACCTGGAGCCCTGCACCGGTACCAG 851
Qy 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
Db 852 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATGCGGCCCCACAGAGAAC 911
Qy 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
Db 912 GGCACGAGCTGCCAGCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGGTGGCGCGTG 971
Qy 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
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Db 1032 GTGGCTTACACGATACCCCATCGTCAAGGCTTCGGGCGGGAGCTGAGCTACGTCTGTG 1091
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Db 1092 CTGGCGGGAATCTTCTGTGTAGCCCATCTCTTCTCATGATCGAGAGCGCGGACCTG 1151
Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1152 GGGACCTGTTCGCTCCGCGCATCTTCTAGGCTCGGCATGAGCATCAGCTACGCGGCC 1211
Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
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Qy 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 1272 GCGCGGCTTTCATCAGCGCGGCTCGCAGCTGGCCATCCTTCTATCTCTCTCTCTCT 1331
Qy 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401

Db 1332 CAGCTGCTCGGCATCTCGGTGTGGTTCTGTGTGGTGGACCCCTCCCACTCGTGGTGGACTTC 1391
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Db 1392 CAGGACCAAGCGGACACTTGACCCCGCTTTGCCAGGGGCGTGTCTCAAGTGGCATCTCG 1451
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 1452 GACCTGTCCCTCATCTGCTGCTGGGCTACAGCATGCTGCTGATGGTCACTGCTACTGTG 1511
Qy 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 1512 TAGCCCATCAAGACCCCGAGGCGTGGCCGAGACCTTCAACGAGGCGCAAGCCCATCGGCTTC 1571
Qy 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
Db 1572 ACCATGTACACCACTGCTGTGTGGCTGGCTTTCATCCCATCTCTTTTGGCACCTCA 1631
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 501
Db 1632 CAGTCAGCGCAAGCTGTATACATCCAGAACACCACTGACTGTCTCGTGAGTCTGAGC 1691
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
Db 1692 GCTTCAGTGTCCCTGGGGATGCTCTACATGCCAAAGTCTACATCATCTCTTCCACCCG 1751
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 1752 GAGCAGAACCTGGCCAAAGCGCAGCTCTCAAGCCCGTGGTCAAGCCCGCCACCATG 1811
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 1812 TCCAAACAGTTTACACAGAGGGGCACTTCAGGCCCAATGGGAGGACCAATCAGAGCTG 1871
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrAsn 581
Db 1872 TGTGAGAACCTGGAGACCCGAGCGTGGCTACCAACAGACCTACGTACCTACCTACCAAC 1931
Qy 582 HisAlaIle 584
Db 1932 CATGCCATC 1940

RESULT 2
PCT-US91-09422-18
; Sequence 18. Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481

; FILING DATE: 30-JAN-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/626,806
 ; FILING DATE: 12-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-6PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4095 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: SN30
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 463..3198
 ; PCT-US91-09422-18

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 Best Local Similarity: 91.67% Mismatches: 1
 Query Match: 98.18% Indels: 53
 DB: 5 Gaps: 1

US-10-828-332-7 (1-584) x PCT-US91-09422-18 (1-4095)

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DB	1351	GCTCGCAGGGCCACACGACCGGCACCTCTCTTTGGATGGGTCTGTATAGCTGGGGCTCC	1410
QY	14	-----14	
DB	1411	AAGAGTGCCCTGTGCTGGCCTTGAGAGGTGGCGGCGCAGTCACCATCTCCCC	1470
QY	15	-----GlyPheAspArgTyrPheSerSerArgThrIleuAspAsnAn	28
DB	1471	AAGAGGATGTCTGTTGAGGGTTCCACCGATACTTCTCCAGCGCCAGCTGGACCAAC	1530
QY	29	ArgArgAsnIleTTPheAlaGluPheTTPGluAspAsnPheHisCysLysLeuSerArg	48
DB	1531	AGCGCGCAACATCTGGTTTCCGAGTCTGGAGGACCACTTCATTTGCAAGTTGAGCCGC	1590
QY	49	HisAlaLeuLysGlySerHisIleLysLysCysThrAsnArgGluArgIleGlyGln	68
DB	1591	CACGCGCTCAAGAGGAAGCCACATCAAGAAAGTCACCAACCGAGAGCGCATCGGGCAG	1650
QY	69	AspSerAlaTyrGluGlnGluLysValGlnPheValIleAspAlaValTyrAlaMet	88
DB	1651	GACTCGGCTATGAGCAGGAGGGGAGGTGCAGTTCTGTTGATTCAGCGCTGTGTACGCCATG	1710
QY	89	GlyHisAlaLeuHiAlaMetHisArgAspLeuCysProGlyArgValGlyLysCysPro	108
DB	1711	GGCCAGCGCTGACGCCATGACCGTGCCTGTGTCGGCGCGGTAGGACTCTGCCCT	1770
QY	109	ArgMetAspProValAspGlyThrGlnLeuLeuLysTyrIleArgAsnValAsnPheSer	128
DB	1771	CGCATGGACCCCGTGGATGGCCAGCCAGCTGCTTAAGTACATCAGGAACGTCAACTTCA	1830
QY	129	GlyIleAlaGlyAsnProValThrPheAsnGluAsnGlyAspAlaProGlyArgTyrAsp	148

DB	1831	GGCATTGGGGGAACCTGTAACTTCAATGAGAACGAGACGACCGGGGGCTACGAC	1890
QY	149	IleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyrLysValIleGlySerTrpThr	168
DB	1891	ATCTACCAAGTACCAACTCGCAATGGCTCGGCGGAGTACAAGGTTCATCGCTCGTGACA	1950
QY	169	AspHisLeuHisLeuArgIleGluArgMetGlnTTPProGlySerGlyGlnGlnPro	188
DB	1951	GACCACCTGCACCTCAGAAATAGAGCGGATGAGTGGCCAGGAGTGGCCAGCAGCTGCCG	2010
QY	189	ArgSerIleCysSerLeuProCysGlnProGlyGluArgLysGlyThrValLysGlyMet	208
DB	2011	CGCTCATCTGCAGTCTGCCCTGCCAGCCCGGGGAGCGAAGAGACTGTGAAGGCATG	2070
QY	209	AlaCysCysTTPHisCysGluProCysThrGlyTyrGlnTyrGlnValAspArgTyrThr	228
DB	2071	GCTTGCTGCTGGCACTGGAGCCCTGCACCGGATACCAAGTGGACCGCTACACC	2130
QY	229	CysLysThrCysProTyrAspMetArgProThrGluAsnArgThrSerCysGlnProIle	248
DB	2131	TGTAAGACCTGCCCTACGACATGCGGCCCAAGAGAACCGCAGGCTGCCAGGCCATC	2190
QY	249	ProIleValLysLeuGluTTPAspSerProTTPAlaValLeuProLeuPheLeuAlaVal	268
DB	2191	CCCATCTGCAAGTTGGAGTGGGACTCGCGGTGGGCGGTGCTGCCCTCTTCTTGGCCGTG	2250
QY	269	ValGlyIleAlaAlaThrLeuPheValValThrPheValArgTyrAsnAspThrPro	288
DB	2251	GTGGCATCGCGCCGACGCTGTTCGTGGTGGTTCACGTTTGTGCGGTACACGATACCCCC	2310
QY	289	IleValLysAlaSerGlyArgGluLeuSerTyrValLeuLeuAlaGlyIlePheLeuCys	308
DB	2311	ATCGTCAAGGCTCGCGCGGAGCTGAGTACGTGCTGTCGGCGGCGATCTTCTGTGTC	2370
QY	309	TyrAlaThrThrPheLeuMetIleAlaGluProAspLeuGlyThrCysSerLeuArgArg	328
DB	2371	TAGCCCATCTCTCTCTCATGATCGCAGCGCGGACCTGGGACCTGTCGCTCGCCCGC	2430
QY	329	IlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAlaLeuLeuThrLysThrAsnArg	348
DB	2431	ATCTTCTAGGCTCGGCATGAGCATCAGTACGCGGCGCTGCTCACCAAGACCAACGC	2490
QY	349	IleTyrArgIlePheGluGlnGlyArgSerValSerAlaProArgPheIleSerPro	368
DB	2491	ATTTACCGCATCTTTGAGCAGCGCAACCGTGGTCACTGCGCGCGCTTTCATCAGCCCG	2550
QY	369	AlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeuGlnLeuLeuGlyIleCysVal	388
DB	2551	GCCTCGCAGCTGGCCATCACCCTTCATCTCATCTCCCTGCAGCTGCTCGGCATCTGCGTG	2610
QY	389	TrpPheValValAspProSerHisSerValValAspPheGlnAspGlnArgThrLeuAsp	408
DB	2611	TGTTGTTGGTGGACCCCTCCACCTCGGTGGTGGACTTCCAGGACCAACGAGACCTTGAC	2670
QY	409	ProArgPheAlaArgGlyValLeuLysCysAspIleSerAspLeuSerLeuIleCysLeu	428
DB	2671	CCCCCTTTGCGAGGGCGTCTCAAGTGCAGCATCTCGGACCTGCTCCCTCATCTGCGCTG	2730
QY	429	LeuGlyTyrSerMetLeuLeuMetValThrCysThrValTyrAlaIleLysThrArgGly	448
DB	2731	CTGGCTACAGATGCTGCTGATGTCACGTGTACTGTGTACGCCATCAAGACCCGAGGC	2790
QY	449	ValProGluThrPheAsnGluAlaLysProIleGlyPheThrMetTyrThrThrCysIle	468
DB	2791	GTGCCGAGACCTTCAACGAGGCCAAGCCCATCGGCTTCCACCATGTACACCACTGCATT	2850
QY	469	ValTrpLeuAlaPheIleProIlePhePheGlyThrSerGlnSerAlaAspLysLeuTyr	488
DB	2851	GTCTGGCTGGCTTTCATCCCATCTTTTGGACCTCACAGTCAAGCCGACCAAGCTGTAC	2910
QY	489	IleGlnThrThrThrThrValSerValSerLeuSerAlaSerValSerLeuGlyMet	508
DB	2911	ATCCAGAACACCACTGACGCTCTCCGTGAGTCTGAGCGCTTTCAGTGTCTCTGGGGATG	2970

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QY 509 LeuTyrMetProLysValTyrIleLeuPheHisProGluGlnAsnValProLysArg 528
Db 2971 CTCATACATGCCCCAAGATCTACATCATCTCTTCACCCGGAGCAGAACGTGCCCAAGCGC 3030
QY 529 LysArgSerLeuLysAlaValValThrAlaAlaThrMetSerAsnLysPheThrGlnLys 548
Db 3031 AAGCGCAGTCTCAAAAGCGTGGTCCACCGCCGCCACCATGTCTCAACAAGATTCCACACAGAG 3090
QY 549 GlyAsnPheArgProAsnGlyGluAlaLysSerGluLeuCysGluAsnLeuGluThrPro 568
Db 3091 GGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTGTGTGAGAACCTTGGAGACCCCA 3150
QY 569 AlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsnHisAlaIle 584
Db 3151 CGCTGGCTACCAACAGACCTACGTCACTACACCAACCATGCCATC 3198

RESULT 3
US-08-617-785-1
; Sequence 1, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2736)
US-08-617-785-1

Alignment Scores:
Pred. No.: 0 Length: 2736
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 3 Gaps: 1

US-10-828-332-7 (1-584) x US-08-617-785-1 (1-2736)
QY 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 988 GGTGCTGTACGATCCTCCCAAGAGGATGTCCTGACGAGGCTTCGACCGCTACTTCTCC 1047
QY 22 SerArgThrLeuAspAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
Db 1048 AGCGCGACGTGGCAACAACCGCGCAACATCTGTTTGGCGATTTCTGGAGAGCAAC 1107
QY 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
Db 1108 TTCACATGCAAGCTGAGCGCCGACGCTCAAGAGGAGGCGACGACGTCAGAGTGCACC 1167
QY 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
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82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
1228 ATCGATGCCGTGTACGCCATGGGCCACGCGCTGCACGCCATGCACCGTGCCTGTGTGTCCC 1287
102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
1288 GGCGCGTGGGGCTCTGCCCGCGCATGAGCCCTGTAGATGGCACCCAGCTGCTTAAGTAC 1347
122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
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142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
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162 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
1468 AAGGTCAATTGGCTCTCGACTGACCACTGCACCTTAGAATAGACGCGATGCACCTGGCG 1527
182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
1528 GGGAGCGGCGAGCAGCTGCCCGCTCCATCTGCAGCCCTGCCCTGCCCAACCGGGTGAGCG 1587
202 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
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242 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
1708 CGCACGGGCTGCCGGCCCATCCCATCAAGCTTGAGTGGGGCTGCCCTGGGGCCGTG 1767
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1768 CTGCCCCCTCTTCTTGGCCGCTGGTGGCATCGCTCCACGTTGTTCGTGGTGATCACCTTT 1827
282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
1828 GTGGCTTACAAACGACACGCCCATCGTCAAGSCCTCGGGCGTGAACCTAGCTAGCTGCTG 1887
302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
1888 CTGGCAGGCATCTTCTGTGTCTATGCCACCATCTCCATGATCGCTGAGCCGACCTT 1947
322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
1948 GGCACCTGCTGCTGCGCCGGAATCTTCTGGGACTAGGGATGACATCAGCTATGACGCC 2007
342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
2008 CTGCTCACAAGACCAACCGCATCTACCGCATCTTCGAGCAGGCGCAAGCGCTCGTCA 2067
362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
2068 GCCCAGCTTCATCAGCCCGCTCAGCTGAGTGGCCATCACCTTTCAGCCTCATCTCGGTG 2127
382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
2128 CAGTGTGTGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2187
402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
2188 CAGGACCGCGGACACTCGACCCCGCTTCCGACGAGGGGTGTGCTCAAGTGTGACATCTCG 2247
422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
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RESULT 4

US-09-817-464-1
 ; Sequence 0, Application US/09817464
 ; Patent No. 6515107
 ; GENERAL INFORMATION:
 ; APPLICANT: Flor, Peter J.
 ; APPLICANT: Kuhn, Ranier
 ; APPLICANT: Lindaur, Kristen
 ; APPLICANT: Puttner, Irene
 ; APPLICANT: Knopfel, Thomas
 ; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
 ; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
 ; FILE REFERENCE: 4-19679/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/817,464
 ; EARLIER FILING DATE: 2001-03-26
 ; EARLIER APPLICATION NUMBER: US/08/617,785
 ; EARLIER FILING DATE: 1996-03-19
 ; EARLIER APPLICATION NUMBER: EPO 9416553.7
 ; EARLIER FILING DATE: 1994-08-19
 ; EARLIER APPLICATION NUMBER: EPO 93810663.0
 ; EARLIER FILING DATE: 1993-09-20
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO SEQ ID NO 1
 ; LENGTH: 2736
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2736)
 US-09-817-464-1

Alignment Scores:

Pred. No.: 0 Length: 2736
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 96.70% Indels: 1
 Db: 4 Gaps: 1

US-10-828-332-7 (1-584) x US-09-817-464-1 (1-2736)

QY 3 GlyValSerSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
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 Db 988 GGTGTGTACAGATCTCTCCCAAGAGGATGTCGTCACGAGGCTTCGACCGCTACTTCTCC 1047
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 QY 22 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
 |||||
 Db 1048 AGCCGACGCTGGACCAACACCGCGCGCAACATCTGGTTTGGCGAGTTCTGGAGAGCAAC 1107
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Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 2188 CAGGACGAGCGACACTCGACCCCGCTTCGCCAGGGGTGTCTCAAGTGTGACATCTCG 2247
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Qy 442 TyrAlaIleIleThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
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Qy 462 ThrMetTyrThrThrCysIleValTrrPheIleLeuAlaPheIleProIlePheGlyThrSer 481
Db 2368 ACCATGTACACCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2427
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 2428 CAGTCGCGCGCAAGCTGTATCATCCAGACGACGCTGACGCTGCTGCTGCTGCTGCTGCT 2487
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTrrIleIleLeuPheHisPro 521
Db 2488 GCCTCGGTGTCCTGGGAATGCTCTACATGCCAAAGTCTACATCATCTCTTCCACCCG 2547
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 541
Db 2548 GAGCAGACAGCTGCGCAAGCGAAGCGAGCGCTCAAGCGCGTCTACGCGCGCCACCATG 2607
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2608 TCCAAACAGTTCACGCAAGAGGCACTTCGCGCCCAACGAGAGGCGCAAGTCTGAGCTC 2667
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
Db 2668 TGCAGAACCTTGAGCGCCAGCGCTGCCACCAACAGACTTACGTCACTTACACCAAC 2727
Qy 582 HisAlaIle 584
Db 2728 CATGCAATC 2736

RESULT 5

US-09-641-318-1

; Sequence 1, Application US/09641318

; Patent No. 6384205

; GENERAL INFORMATION:

; APPLICANT: BELAGAJE, RAMA M.

; WU, SU

; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN

; AND RELATED NUCLEIC ACID COMPOUNDS

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ELI LILLY AND COMPANY

; STREET: LILLY CORPORATE CENTER

; CITY: INDIANAPOLIS

; STATE: INDIANA

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/641,318

; FILING DATE: 18-Aug-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/816,178A

; FILING DATE: 12-MAR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: GAYLO, PAUL J.

; REGISTRATION NUMBER: 36,808

; REFERENCE/DOCKET NUMBER: X-10579

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (317) 276-0756

; TELEX: (317) 276-3861

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3431 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 26..2761

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-641-318-1

Alignment Scores:

Pred. No.: 0 Length: 3431

Score: 3004.50 Matches: 564

Percent Similarity: 97.77% Conservative: 6

Best Local Similarity: 96.74% Mismatches: 12

Query Match: 96.70% Indels: 1

DB: 3 Gaps: 1

US-10-828-332-7 (1-584) x US-09-641-318-1 (1-3431)

Qy 3 GlyValSerSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 1013 GGTGCTGTACAGTCTCTCCCAAGAGGATTCGCTACGAGGCTTCGACCGCTACTTCTCC 1072
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Db 1073 AGCGCAAGCTTGACAAACAAACCGCGCGCAACATCTGGTTTGGCGAGTTCTGGGAGGACAC 1132
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QY 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 2573 GAGCAGAACGTGCCCAAGCGCAGCGCAGCTTCAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 2632
QY 542 SerAsnLysPheThrGlnLysGlnAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2633 TCCAAACAGTTTCCGAGAGGGGCAACTTTCGCGCCCAACGGAGAGGCGCAAGTCTGAGCTC 2692

QY 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAen 581
Db 2693 TCGGAGAACCTTTGAGCGCCCGCTGGCCGCTGACCAACAGACTTACGTCTACTTACACCAAC 2752
QY 582 HisAlaIle 584
Db 2753 CATGCCATC 2761
RESULT 6
US-09-641-318-3
; Sequence 3, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: GAYLO, PAUL J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-641-318-3
Alignment Scores:
Pred. No.: 0 Length: 3431
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 3 Gaps: 1
US-10-828-332-7 (1-584) x US-09-641-318-3 (1-3431)
QY 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 1013 GGUGUGUCAGUCCUCCCAAGAGGAGUCCCGUACGAGGCUCCGCGUACUUCUCC 1072
QY 22 SerArgThrLeuAspAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAen 41
Db 1073 AGCCGACGCGUGGACACACCGCGCAACAUUGGUUGCGAGUUCUGGAGGACAAAC 1132
QY 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61

RESULT 9
 PCT-US91-09422-20
 ; Sequence 20, Application PC/TUS9109422
 ; GENERAL INFORMATION:
 ; APPLICANT: Mulvihill, Eileen R.
 ; APPLICANT: Hegen, Frederick S.
 ; APPLICANT: Houamed, Khaled M.
 ; APPLICANT: Almer, Wolfhard
 ; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend
 ; STREET: One Market Plaza, Steuart Street Tower
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/09422
 ; FILING DATE: 19911212
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/672,007
 ; FILING DATE: 18-MAR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/626,806
 ; FILING DATE: 12-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-6PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2426 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: SR13
 ; PCT-US91-09422-20

Alignment Scores:

Pred. No.: 4,66e-307 Length: 2426

Score: 2720.50 Matches: 519

Percent Similarity: 90.73% Conservative: 0

Best Local Similarity: 90.73% Mismatches: 1

Query Match: 87.56% Indels: 53

DB: 5 Gaps: 1

US-10-828-332-7 (1-584) x PCT-US91-09422-20 (1-2426)

QY 1 MetProGlyValSerSerSerLeuProThrArgMetThrSer----- 14

DB 542 ATGCCAGGGGTATCATCTTTGGCCACGCGGATGACATC-AGGAGGTGTGTGGAGGCA 600

QY 14 ----- 14

DB 601 GCTCGCAGGGCCACACGACCGCCACCTCTCTTTGGATGGGTCTGTATAGCTGGGGCTCC 560

QY 14 ----- 14

Db 661 AAGAGTGCCTCTGCTGCGCCTTGTAGGAGGTGGCGGCGCAGTCAACATTCTCCCC 720

QY 15 -----GlyPheAspArgTyrPheSerSerArgThrLeuAspAsnAen 28

Db 721 AAGAGGATGCTGTTTCGAGGGTTCACCGATATCTTCTCCAGCGCAGCGCTGGACAAC 780

QY 29 ArgArgAsnIleTTPheAlaGluPheTTPGluAspAsnPhHisCysAlaLeuSerArg 48

Db 781 AGCGCAACATCTGCTTTGCGCAGTTCGGGAGGACAACCTTCATTGCAAGTTGAGCGCC 840

QY 49 HisAlaLeuLeuValGlySerHisIleLeuValCysThrAsnArgGluArgIleGlyGln 68

Db 841 CACGCGCTCAAGAGGAGGACCATCAAGAGTGCACCAACCGAGAGCGCATCGGCGAG 900

QY 69 AspSerAlaTyrGluGlnGluGlyValGlnPheValIleAspAlaValTyrAlaMet 88

Db 901 GACTCGGCTATGACGAGGAGGAGGAGTTCGTTGATTGACGCTGTGTACGCCATG 960

QY 89 GlyHisAlaLeuHisAlaMetHisArgAspLeuCysProGlyArgValGlyLeuCysPro 108

Db 961 GGGCAGCGCTGCGACCGCATGCGCTGACCTGTGTCCCGCGCGGTAGGACTCTGCCCT 1020

QY 109 ArgMetAspProValAspGlyThrGlnLeuLeuValTyrIleArgAsnValAsnPheSer 128

Db 1021 CGCATGGACCCCGTGGATGGCACCCAGCTGCTTAAGTATACATCAGGAACGTCAACTTCTCA 1080

QY 129 GlyIleAlaGlyAsnProValThrPheAsnGluAsnGlyAspAlaProGlyArgTyrAsp 148

Db 1081 GCGATTGGGGGAGACCTGTAACTTCAATGAGAACGAGAGCGCACCGGGGGCGCTACGAC 1140

QY 149 IleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyrLeuValIleGlySerTTPThr 168

Db 1141 ATCTACCAAGTACCAACTCGCAATGGCTCGGCGGAGTCAAGGTATCATCGGCTCGTGACA 1200

QY 169 AspHisLeuHisLeuArgIleGluArgMetGlnTTPProGlySerGlyGlnGlnLeuPro 188

Db 1201 GACCACCTGCACCTCAGAAATAGCGGATGAGTGGCCAGGAGTGGCCAGGAGTGGCGG 1260

QY 189 ArgSerIleCysSerLeuProCysGlnProGlyGluArgLysLysThrValIleGlyMet 208

Db 1261 CGCTCCATCTGCAGTCTGCTCCCTGCGAGCCCGGGGAGCGGAGAGACTGTGAAGGCGCATG 1320

QY 209 AlaCysCysTTPHisCysGluProCysThrGlyTyrGlnTyrGlnValAspArgTyrThr 228

Db 1321 GCTTGTCTGTGCACTGCGAGCCCTGACCGGTACCAAGTACCAAGTGGACCGCTACACC 1380

QY 229 CysLysThrCysProTyrAspMetArgProThrGluAsnArgThrSerCysGlnProIle 248

Db 1381 TGTAAGACCTGCCCTACGACATGCGGCCCAACAGAGAACCGCACGAGTGGCCAGCCATC 1440

QY 249 ProIleValLysLeuGluTTPAspSerProTTPAlaValLeuProLeuPheLeuAlaVal 268

Db 1441 CCCATCGTCAAGTGGAGTGGGACTCGCGCGTGGCGGCTGTGCTGCCCTCTTCTTGGCGGTG 1500

QY 269 ValGlyIleAlaAlaThrLeuPheValValThrPheValArgTyrAsnAspThrPro 288

Db 1501 GTGGGCAATCGCGCCGCGCTGTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

QY 289 IleValLysAlaSerGlyArgGluLeuSerTyrValLeuLeuAlaGlyIlePheLeuCys 308

Db 1561 ATCGTCAAGGCTCGGGCGGAGCTGAGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

QY 309 TyrAlaThrThrPheLeuMetIleAlaGluProAspLeuGlyThrCysSerLeuArgArg 328

Db 1621 TAGCGCATCTCTCTCTATATCGCAGAGCGGAGCTGGGAGCTGTGCTGCTGCTGCTGCTGCT 1680

QY 329 IlePheLeuGlyLeuGlyMetSerIleTyrAlaAlaLeuLeuThrIleThrAsnArg 348

Db 1681 ATCTTCTTAGGGCTCGGCATGAGCATGAGTACGCGGCGCTGCTGACCAAGACCAACCGC 1740

QY 349 IleTyrArgIlePheGluGlnGlyArgSerValSerAlaProArgPheIleSerPro 368

Db 1813 GTGCTGTGTTTGTTCATATATTGGAAATCATCGCCACACACTTTGTGTGTCGTGACCTTT 1872
Qy 282 ValArgTyrAsnAspThrProIleValIleValSerGlyArgGluLeuSerTyrValLeu 301
Db 1873 GTCCGCTAATGACACACTATCGTGAGGCTTCAGGACGCACTTAGTTAGTGTCT 1932
Qy 302 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 321
Db 1933 CTAACGGGGATTTTCTCTGTTATTCAATCAGCTTTTAAATGATTGCAGCACCAGATACA 1992
Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1993 ATCATATGCTCTTCGACGGGTCTTCAGGACTTGGCATGTGTTTCAGCTATGAGCC 2052
Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyArgSerValSer 361
Db 2053 CTTCGACCAAAACAAACGATCCACCGAATATTGACGAGGGAAGAAATCTGTACA 2112
Qy 362 AlaProArgPheIleSerProIleSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 2113 GCGCCCAAGTTCATTAGTCCAGCATCTCAGCTGGTGATCACCTTCAGCCTCATCTCCGTC 2172
Qy 382 GlnLeuLeuGlyIleCysValThrPheValValAspProSerHisSerValValAspPhe 401
Db 2173 CAGCTCCTGGAGTGTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2232
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 2233 CGAGCAGCGGACACTAGATCCAGAGAGCGGAGTGTCTCAAGTGTGACATTTCT 2292
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 2293 GATCTCTCACTATTGTTTCACTTGGATACAGTATCTCTTGTATGTCATCTGTTACTGTT 2352
Qy 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 2353 TATGCCAATAAAGCAGAGGTGTCCAGAGACTTTCAATGAAGCCAAACCTATTGGATT 2412
Qy 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
Db 2413 ACCATGTATACCACTGCATCATTTGGTGTGTTTTCATCCCATCTTTTGTGTACGCC 2472
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
Db 2473 CAGTCAGCAGAAAGATGTACATCCAGACAACTTACTGTCTCTCCATGAGTTAAGT 2532
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 521
Db 2533 GCTTCAGTATCTCTGGCATGCTCTATATGCCAAGGTTTATATATATTTTTCATCCA 2592
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 2593 GAACAGATGTTCAAAAGCAGAGGAGCTTCAAGGCTGTGTGTGACAGCTGCCACCATG 2652
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2653 CAAAGCAAACTGATCCAAAAGGAAATGACAGACCAATGGCGAGTGGAAGTGAACCTC 2712
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
Db 2713 TGTGAGAGCTTTGAAACCAACACTCTCTCTACCAAGACATATATATGTTTACAGCAAT 2772
Qy 582 HisAlaIle 584
Db 2773 CATTCAATC 2781

RESULT 11

US-08-855-146-3

; Sequence 3, Application US/08855146

; Patent No. 6221609

; GENERAL INFORMATION:

; APPLICANT: Belagaje, Rama M.

; APPLICANT: Wu, Su

; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Department
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,146
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,243
; FILING DATE: 07-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10836
; TELEPHONE: (317) 276-6334
; TELEFAX: (317) 276-2764
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; US-08-855-146-3

Alignment Scores:

Pred. No.:	7,77e-266	Length:	3321
Score:	2370.00	Matches:	437
Percent Similarity:	84.91%	Conservative:	58
Best Local Similarity:	74.96%	Mismatches:	86
Query Match:	76.28%	Indels:	2
DB:	3	Gaps:	2

US-10-828-332-7 (1-584) x US-08-855-146-3 (1-3321)

Qy 3 GlyValSerSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
Db 1036 GGGGCGUGACAAUUUUGCCCAACGACCAUAUUGAUGAUUUGAUGCAUUCUUAUA 1095
Qy 22 SerArgThrLeuAspAsnArgArgAsnIleTTPheAlaGluPheTrpGluAspAsn 41
Db 1096 AGCCGAACUUCUCCCAUAUUGAAGAAUUGUGUGUUUGCAGAAUUCUGGGAGGAUAU 1155
Qy 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
Db 1156 UUGGCGUCAGUUGAUGAUCACUAGGG---AAAAGNACAGCAUAUAAAAGAAUAGCACA 1212
Qy 62 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGlnGlyLysValGlnPheVal 81
Db 1213 GGGCUGGAGCGAAUUGCUGCGGAUUCUUAUGAACAGGAAGGAAGGCAUUCUUAUGUA 1272
Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 1273 AUUGAUGCUGUAUUAUCCCAUGGCTUACGCCUCCCAUUAUUGCAAAAGAUUCUGCCCU 1332
Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr 121
Db 1333 GGAUACAUGGCCUUUGUCCAGGAUGAGUACCAUUGAUGGGAAGAGACGACUUGGUUAU 1392
Qy 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141

Db 1393 AUUCGGGCGUAAUUUAUAGGCGAGUGCGCACUCCUGUCACUUUUUAUAGAAACCGGA 1452
Qy 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
Db 1453 GAUGCUCUGGACGUAUGAUUAUCUCCAGUAUCAAUAACAAACAAAGACACAGAGUAC 1512
Qy 162 LysValIleGlySerTyrThrAspHisLeuHisLeuArgIleGluArgMetGlnTyrPro 181
Db 1513 AAAGUCAUGCGCCACUGAGCAACUACAGCUUUAUAAAGUGGAGAGAGCAUAGCAGUGGCGU 1572
Qy 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
Db 1573 CAUAGAGAACAUAUCUACCCGCGUCUGUCAGCGUCGCGUGUAAGCCAGGCGAGAGG 1632
Qy 202 LysIleThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 221
Db 1633 AAGAAACCGUGAAGGGGUCUUCUGUGUGGCGACUUGAGAACGUGUAGAGGUUACAAAC 1692
Qy 222 TyrGlnValAspArgTyrThrCysIleThrCysProTyrAspMetArgProThrGluAsn 241
Db 1693 UACGAGGUGAGAGCUGUCUGGUAACUUUGCCUUGGAUCAGAGACCCAAACAUAGAAC 1752
Qy 242 ArgThrSerCysGlnProIleValLysLeuGluTyrAspSerProTyrAlaVal 261
Db 1753 CGCAGCGCUGCCAGCUUAUCCCAUCAAAUUGAGUGGCAUUCUCCUGGCGUGUG 1812
Qy 262 LeuProLeuPheLeuAlaValValGlyIleAlaIleThrLeuPheValValValThrPhe 281
Db 1813 GUGCUGUGUUGUUGCAUAUAGGAAUAUCUCCAGCCACCAUUCUGUGAGUGAGCCUUU 1872
Qy 282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 1873 GUCCGCUAAUAGACACACUUCUGGAGGCGUUCAGGACCGCAACUUGUUAUGUGUCUC 1932
Qy 302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
Db 1933 CUACGGGGAUUUUUCUUGUAUUAUCAACGCUUUUAUAGUAGCAGCACCAGAUACA 1992
Qy 322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
Db 1993 AUCAUAUGCUCUUCGCGAGGUGUUCUCCUAGGACUUGGCAUGUGUUAUGCAGCAGCC 2052
Qy 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyArgSerValSer 361
Db 2053 CUUCUGACCAAAACAAACCGUAUCCGGAUUAUUGAGCAGGGAAGAAUUCUGUCACA 2112
Qy 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db 2113 GCGCCCAAGUUAUUAUGCAGCAUCUCCAGUGGUAUCCUUCAGCCUUCUCCUGUC 2172
Qy 382 GlnLeuLeuGlyIleCysValTyrPheValValAspProSerHisSerValValAspPhe 401
Db 2173 CAGCUCUUGAGUGUUGUCUGUUGUUGUUGAUUCCGCCCAUUAUUAUUAUUAUUAU 2232
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
Db 2233 GGAGAGCAGCGACACUAGUCCAGAGAACGCGAGGAGGUGUCCUAGUGUGACAUUUUCU 2292
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
Db 2293 GAUCUCUACAUUUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2352
Qy 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 2353 UAUGCCAAUAAACGAGAGGUGUCCAGAGCUUUAUUAUUAUUAUUAUUAUUAUUAU 2412
Qy 462 ThrMetTyrThrThrCysIleValTyrPheAlaPheIleProIlePhePheGlyThrSer 481
Db 2413 ACCAUGUAUACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2472
Qy 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501

Db 2473 CAGUCAGCAGAAAAGAUAGUAUCCAGACAACAACUACUACUGUCUCCAGAGUUUAAGU 2532
Qy 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
Db 2533 GCUUCAGUAUUCUGGCGAUGUCUUAUAGCCCAAGSUUAUUAUUAUUAUUAUUAUUAU 2592
Qy 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
Db 2593 GAACAGAUAUUCAAAACCAAGAGAGGAGGCUCAAGGCGUGGUGGACAGCUGCCACCAUG 2652
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
Db 2653 CAAGCAAAACUGAUCUCCAAAAGGAAUAGACAGACCAAAUUGCGAGGUGAAAGUAGACUC 2712
Qy 562 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 581
Db 2713 UGUGAGAGUCUUGAAACCAACACUUCUCCUCCAAACAACAUAUAUACAGUUAACAGCAU 2772
Qy 582 HisAlaIle 584
Db 2773 CAUCAAUC 2781

RESULT 12
US-08-823-110-2
; Sequence 2, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-823-110-2

Alignment Scores: 3,74e-263 Length: 3833
Pred. No.:

Score: 2348.00 Matches: 438
Percent Similarity: 82.56% Conservatives: 59
Best Local Similarity: 72.76% Mismatches: 84
Query Match: 75.57% Indels: 21
DB: 3 Gaps: 3

US-10-828-332-7 (1-584) x US-08-823-110-2 (1-3833)

QY 3 GlyValSerSerLeuProThrArgMetThr---SerGlyPheAspArgTyrPheSer 21
DB 1494 GGGGGTGTGACAAATTTGGCCAAACGAGCATCAATATGATGGATTTGATCGATCTTTAGA 1553
QY 22 SerArgThrLeuAspAsnAsnArgAsnIleTTPheAlaGluPheTTPGluAspAsn 41
DB 1554 AGCCGAACCTCTGGCCAAATATCGAAGAAATGTGTGTTGCGAATTTCTGGGAGAGAAAT 1613
QY 42 PheHisCysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
DB 1614 TTTGGCTGCAGTTAGGATCATATGGG---AAAGGAACAGTCATATAAAGAAATGCACA 1670
QY 62 AsnArgGluArgIleGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
DB 1671 GGGCTGGAGCGAATTTGCTCGGCAATCATCTTATGAACAGGAAGGAAGGTCCAAATTTGTA 1730
QY 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
DB 1731 ATTGATGCTGTATATTCATGCTTACGCCCTGCACAAATATGCACAAAGATCTCTGCCCT 1790
QY 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
DB 1791 GGATACATTTGGCTTTGTCAGCAATGAGTACATTTGATGGGAAGAGCTACTTGGTTAT 1850
QY 122 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
DB 1851 ATTGGGCTGTAAATTTTAAATGGCAGTGTGTCACCTCTGTCATTTTAAATGAACCGA 1910
QY 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
DB 1911 GATGCTCTCGACGTTATGATATCTTCCAGTATCAATTAACCAACCAAGACAGAGTAC 1970
QY 162 LysValIleGlySerTyrThrAspHisLeuHisLeuArgIleGluArgMetGlnTyrPro 181
DB 1971 AAGTTCATCGGCACCTGACCAATCAGCTTTCATCTAAGTGTGAAGACATGACGTGGCT 2030
QY 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
DB 2031 CATAGAACATACCTCACCGCGCTGTCTCAGCGCTGCCGTGTGAAGCAGGGAGAGG 2090
QY 202 LysLysThrValLysGlyMetAlaCysCysTTPHisCysGluProCysThrGlyTyrGln 221
DB 2091 AAGAAAACGGTGAAGGGGCTCTGCTGCTGCGCACGTGTGAACGCTGTGAAGGTACAA 2150
QY 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
DB 2151 TACCAGGTGGATGAGCTGCTGTGAACCTTTGCCCTCTGGATCAGAGACCCCAACATGAAC 2210
QY 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTyrAspSerProTyrAlaVal 261
DB 2211 CGCAGAGCTGCAGCTTATCCCATCATCAATTTGGAGTGGCATCTCCCTGGGCTGTG 2270
QY 262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
DB 2271 GTGCCCTGTGTTGTGCAATATTTGGAAATCATCGCCACCCACCTTTGTGATCGTGACCTT 2330
QY 282 ValArgTyrAspAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
DB 2331 GTCCGCTATAATGACACACCTATCGTGGGGCTTACGAGCGGCACTTAGTTACGTGCTC 2390
QY 302 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 321
DB 2391 CTAAACGGGATTTTCTCTGTTATTCATCAGCTTTTAAATGATTCAGCACCACATACA 2450
QY 322 GlyThrCysSerLeuArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341

DB 2451 ATCATATGCTCTCTCCGAGCGGTCTTCTAGAGACTTGGCATTTGTTTACGTATGAGCC 2510
QY 342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
DB 2511 CTTCTGACCAAAACAAACCGTATCCACCGAATATTTGAGCAGGGGAAGAAATCTGTCA 2570
QY 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
DB 2571 GCGCCAAAGTTCAATTAGTCCAGCATCTCAGCTGGTGATCACCTTCAGCCCTCATCTCCGTC 2630
QY 382 GlnLeuLeuGlyIleCysValTTPheValValAspProSerHisSerValValAspPhe 401
DB 2631 CAGCTCCCTTGAGTGTGTTGCTGGTGTGTTGGATCCCCCATCATCATCAATGACTAT 2690
QY 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
DB 2691 GGAGAGCAGCGGACACTAGATCCAGAGAAGCCAGGGAGTGTCTCAAGTGTGCATTTCT 2750
QY 422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
DB 2751 GATCTCTCACTCATTTGTTCACTTGGATACAGTATCTCTTGTATGCTCACTTGTACTGT 2810
QY 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
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QY 462 ThrMetTyrThrThrCysIleValTTPheAlaPheIleProIlePhePheGlyThrSer 481
DB 2871 ACCATGATATACCATCTGTCATCATTTGGTGTAGCTTTTCCATCCCATCTTTTGTGACAGCC 2930
QY 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 501
DB 2931 CAGTCAGCAAAAGATGTACATCCAGACAACACACTTACTGTCTCTCCATGAGTTAAGT 2990
QY 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521
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QY 522 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 541
DB 3051 GAACAGATGTTCAAAACGCAAGAGAGCTTCAAGGCTGTGTGACAGCTGCCACCATG 3110
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DB 3111 CAAGCAAACTGTATCAAAAGGAAATGACAGACCAATGGCAGGTGAAAAGTGAATC 3170
QY 562 CysGluAsnLeuGluThrProAla----- 569
DB 3171 TGTGAGAGTCTTGAACCAACAGTAAGTCATCTGTAGAGTTTCCGATGGTCAAGAGCGG 3230
QY 570 -----Leu-AlaThrLysGlnThrTyrValThrTyrThrAsnHisAl 583
DB 3231 AGCACTTCTAATAGATCTTCTCTACCAAGACACATATATCATGTTACAGCAATCATTC 3290
QY 583 aile 584
DB 3291 AATC 3294

RESULT 13
US-08-604-298-2
; Sequence 2, Application US/08604298
; Patent No. 6084084
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/604,298
 FILING DATE: February 21, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 212/044
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3833 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-604-298-2

Alignment Scores:
 Pred. No.: 3,746-263 Length: 3833
 Score: 2348.00 Matches: 438
 Percent Similarity: 82.56% Conservative: 59
 Best Local Similarity: 72.76% Mismatches: 84
 Query Match: 75.57% Indels: 21
 DB: 3 Gaps: 3

US-10-828-332-7 (1-584) x US-08-604-298-2 (1-3833)

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162 LysValIleGlySerThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 181
1971 AAAGTCATCGGCCACTGGACCAATCAGCTTCATCTAAAGTGGGAAGCATGCGATGGGCT 2030

182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
2031 CATAGAGAACATACTCACC GGCGTCTGTCTGCAGCCTCGGTGTAGCCAGGAGGAGG 2090

202 LysLysThrValLysGlyMetAlaCysCysThrHisCysGluProCysThrGlyTyrGln 221
2091 AAGAAAACGGTGAAGGGGCTCTGCTGCTGGCACTGTGAACGCTGTGAAGGTTACAAC 2150

222 TyrGlnValAspArgTyrThrCysLysThrCysAspTrpAspMetArgProThrGluAsn 241
2151 TACCAGGTGGATGAGCTGTCTGTGAACCTTTGGCCCTCTGGATCAGAGACCCCAACATGAAC 2210

242 ArgThrSerCysGlnProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
2211 CGACAGGCTGCCAGCTTATCCCAATCATCAATTGGAGTGGCATTTCTCCCTGGGCTGTG 2270

262 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 281
2271 GTGCTGTGTTGTTGTCATATTGGGAATCATGCCACCACCTTTGTGTGATCGTGACCTTT 2330

282 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
2331 GTCCGCTATAATGACACACCTATCGTGAGGCTTCAGGACGCGAATCTAGTTAGTGTGCTC 2390

302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
2391 CTAAAGGGGATTTTCTCTGTTATTCATCAGCTTTTATGATGAGCAGCAGATACA 2450

322 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 341
2451 ATCATATGCTCCTTCCGACGGTCTTCTAGGACTTGGCATGTGTTTCAGCTATGCGGCC 2510

342 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 361
2511 CTTCTGACCAAAACAAACCGTATCCACCGAATATTTCAGCAGGGGGAAGAATCTGTGACA 2570

362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
2571 GCGCCCAAGTTTCATTAGTCCAGCATCTCAGCTGGTGATCACCTTCAGCCTCATCTCCGTC 2630

382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
2631 CAGCTCCTTGGAGTGTGTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2690

402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
2691 GGAGAGCAGCGGACACTAGATCCAGAGAGGCCAGGGAGTGTCTCAAGTGTGACATTTCT 2750

422 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 441
2751 GATCTCTCACTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2810

442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
2811 TATGCCATTAACAGAGAGGTGTCAGAGACTTTCAATGAAGCCAAACCTATTGGATTT 2870

462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
2871 ACCATGTATACCACTGCATCATTTGGTTAGCTTTCATCCCATCTTTTGGTACAGCC 2930

482 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 501
2931 CAGTCACAGAAAGATGTATCATCCAGACAAACACTTACTGTCTCATGAGTTTAAGT 2990

502 AlaserValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 521

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Db 3051 GAACAGATGTTCAAAACGCAAGAGGAGCTTCAAGGCTGTGTGACAGCTGCCACCATG 3110
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Db 3111 CAAAGCAAACTGATCCAAAGAGAAATGACAGACCAAAATGGCGAGGTGAAAAGTGAACCTC 3170
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Db 3171 TGTGAGAGTCTTGAACCAACAGTAGTATGATCTGTAGAGTTTCCGATGTCGAAGCGGG 3230
Qy 570 -----Leu-AlaThrLysGlnThrTyValThrTyThrAenHisAl 583
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Qy 583 alle 584
Db 3291 AATC 3294

RESULT 14

US-08-823-110-5
; Sequence 5, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-823-110-5

Alignment Scores:

Pred. No.: 4,46e-261 Length: 2724
Score: 2328.00 Matches: 430
Percent Similarity: 85.34% Conservative: 53
Best Local Similarity: 75.97% Mismatches: 81
Query Match: 74.93% Indels: 2
DB: 3 Gaps: 2
US-10-828-332-7 (1-584) x US-08-823-110-5 (1-2724)
Qy 3 GlyValSerSerLeuProThrArgMetThr----SerGlyPheAspArgTyrPheSer 21
Db 979 GGGGCTGTGACAAATTTTCCCAACGAGCATCAATTTGATGGATTTGATCGATCTTTAGA 1038
Qy 22 SerArgThrLeuAspAenAsnArgAsnIleTTPheAlaGluPheTTPheGluAspAen 41
Db 1039 AGCCGAACCTCTTGCCAATAATCGAAGAAATGTGTGGTTTTCAGAAATTTCTGGGAGAGAAAT 1098
Qy 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
Db 1099 TTTGGCTGCAAGTTAGGATCACATGGG---AAAGGAACAGTCATATAAGAAATGCACA 1155
Qy 62 AsnArgGluArgIleGlyLysAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 81
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Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 1216 ATTGATGCTGATATATTCATGCTTACGCCCTTCGCAATATATGCACAAAGATCTCTGCCCT 1275
Qy 102 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr 121
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Qy 142 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 161
Db 1396 GATGCTCTGGACGTTATGATATCTTCAGTATCAATAACCAACAAAGACACAGAGTAC 1455
Qy 162 LysValIleGlySerTTPheAspHisLeuHisLeuArgIleGluArgMetGlnTyrPro 181
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Qy 182 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
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Qy 202 LysLysThrValLysGlyMetAlaCysCysTTPheHisCysGluProCysThrGlyTyrGln 221
Db 1576 AAGAAAACGGTGAAGGGGTCCTTGTCTGTGGCACTGTGAACGCTGTGAAGGTTTACAAC 1635
Qy 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAen 241
Db 1636 TACCAGGTGGATGAGCTGTCTGTGAATTTTGGCCCTCTGGATCAGAGACCCCAACATGAAC 1695
Qy 242 ArgThrSerCysGlnProIleProIleValLysLeuGluTyrAspSerProTyrAlaVal 261
Db 1696 CGCACAGCTGCCAGCTTATCCCATCATCAATTTGGAGTGGCATTTCTCCCTGGGCTGTG 1755
Qy 262 LeuProLeuPheLeuAlaValIleAlaIleAlaThrLeuPheValValThrPhe 281
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Qy 282 ValArgTyrAenAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 301
Db 1816 GTCCGCTATATATGACACCTTATCGTGGAGCTTTCAGGACCGCACTTAGTTACGTGCTC 1875
Qy 302 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 321
Db 1876 CTAAGGGGATTTTCTCTGTATTATCAATCATCGTTTNTATGATTGACGACCAATACA 1935

Qy 322 GlyThrCysSerLeuArgArgGilePheLeuGlyMetSerIleSerTyAlaAla 341
Db |||||
1936 ATCATATGCTCTTCCCGAGGGTCTTCTAGGACTTGGCATGTCTTTTCAGCTATGCAGCC 1995
Qy 342 LeuLeuThrLysThrAsnArgIleTyArgIlePheGluGlnGlyLysArgSerValSer 361
Db |||||
1996 CTTCTGACCAAAACAAACCGTATCCACCGAATATTGAGCAGGGGAGAAATCTGTGCACA 2055
Qy 362 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 381
Db |||||
2056 GCGCCCAAGTTCATAGTCCAGCATCTCAGCTGGTGATCACTTCAGCCTCATCTCCGTC 2115
Qy 382 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 401
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2116 CAGCTCTTGAGGTGTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2175
Qy 402 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 421
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2176 GGAGAGCAGCGGACACTAGATCCAGAGAGCCAGGGAGGTGCTCAAGTGTGACATTTCT 2235
Qy 422 AspLeuSerLeuIleCysLeuLeuGlyTySerMetLeuLeuMetValThrCysThrVal 441
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2236 GATCTCTCACTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2295
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Db |||||
2296 TATGCCATTAAACGAGAGGTGTTCCAGAGACTTTCATGAAGCCAAACCTATTGGATT 2355
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2356 ACCATGTATACCACTGTCATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2415
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2416 CAGTCAGCAGAAAAGATGTATCATCCAGACAAACACTTCTGCTCCATGAGTTTAAGT 2475
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2536 GAACAGAGATGTTCAAAACGCAAGAGGAGCTTCAAGGCTGTGTGTGACAGCTGCCACCATG 2595
Qy 542 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 561
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2596 CAAGCAAACTGATCCAAAAGGAAATGACAGACCAAAATGGCGAGGTGAAAAGTGAATC 2655
Qy 562 CysGluAsnLeuGluThr 567
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2656 TGTGAGAGTCTTGAACC 2673

RESULT 15

US-08-604-298-5

; Sequence 5, Application US/08604298

; Patent No. 6084084

; GENERAL INFORMATION:

; APPLICANT: Stormann, Thomas M.

; APPLICANT: Simin, Rachel T.

; APPLICANT: Hammerland, Lance G.

; APPLICANT: Fuller, Forrest H.

; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC

; TITLE OF INVENTION: GLUTAMATE RECEPTOR

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,298
; FILING DATE: February 21, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-604-298-5

Alignment Scores: 4.46e-261 Length: 2724
Pred. No.: 2328.00 Matches: 430
Score: 85.34% Conservat: 53
Percent Similarity: 75.97% Mismatches: 81
Best Local Similarity: 74.93% Indels: 2
Query Match: 3 Gaps: 2
DB:

US-10-828-332-7 (1-584) x US-08-604-298-5 (1-2724)

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Db |||||
1039 AGCGAACTCTCGCAATAATCGAAGAAATGTGTGGTTTGCAGAAATCTCGGAGGAGAAAT 1098
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Db |||||
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1336 ATTGGGCTGTAAATTTTATGGCAGTGTGGCACTCTGTCTCTTTTATGAAAACCGA 1395
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Db |||||
1396 GATGCTCTGGACGTTATGATATCTTCAGTATCAATAACCAACAAAGACACAGAGTAC 1455
Qy 162 LysValIleGlySerTrpThrAspHisLeuArgIleGluArgMetGlnTrpPro 181
Db |||||
1456 AAAGTCATCGGCCACTGGACCAATCAGCTTCTATAAAGTGGAGACATCGAGTGGGCT 1515

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Qy 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
Db 1516 CATAGAGAAACATACTCACCGGGCTGTCTGTCAGGCTGCGGTGTAAGCCAGGGAGAGG 1575
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Db 1576 AAGAAACGGTGAAGGGGTCCTTGTCTGTCGCACTGGAACGCTGTGAAGGTTACAAC 1635
Qy 222 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 241
Db 1636 TACCAGGTGGATGAGCTGCTGTGAACCTTGGCCCTCTGGATCAGAGACCAACATGAAC 1695
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Db 1756 GTGCCCTGTGTTGTTGCAATATTGGGAATCATGCCACCACCTTTGTGATCGTGACCTTT 1815
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Job time : 333 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 21, 2005, 08:56:12 ; Search time 7314 Seconds
(without alignments)
3868.997 Million cell updates/sec

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Perfect score: 3107
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1	AR381454	AR381454	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
LOCUS	AR381454	AR381454	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
DEFINITION	AR381454	AR381454	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
ACCESSION	AR381454	AR381454	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
VERSION	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
KEYWORDS	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
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ORGANISM	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
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AUTHORS	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
TITLE	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
JOURNAL	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
FEATURES	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
source	AR381454.1	AR381454.1	Sequence 1	from patent US 6608176.	DNA	linear	PAT 18-DEC-2003
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Best Local Similarity:	98.63%	Mismatches:	5
Query Match:	98.18%	Indels:	1
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US-10-828-332-7 (1-584) x AR381454 (1-2838)

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Qy 42 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr 61
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ACCESSION M92077
VERSION M92077.1 GI:205403
KEYWORDS glutamate receptor; metabotropic glutamate receptor.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 3704)
AUTHORS Tanabe,Y., Masu,M., Ishii,T., Shigemoto,R. and Nakanishi,S.
TITLE A family of metabotropic glutamate receptors
JOURNAL Neuron 8 (1), 169-179 (1992)
MEDLINE 92110002
PUBMED 1309649
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DEFINITION Rat metabotropic glutamate receptor (GLUR4) mRNA, complete cds.
ACCESSION M90518
VERSION M90518.1 GI:205400
KEYWORDS metabotropic glutamate receptor.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 4488)
AUTHORS O'Hara,P.J., Sheppard,P.O., Thøgersen,H., Venezia,D.,
Haldeman,B.A., McGrane,V., Houamed,K.M., Thomsen,C., Gilbert,T.L.
and Mulvihill,E.R.
TITLE The ligand-binding domain in metabotropic glutamate receptors is
related to bacterial periplasmic binding proteins
JOURNAL Neuron 11 (1), 41-52 (1993)
MEDLINE 93332699
PUBMED 8338667
REFERENCE 2 (bases 1 to 4488)
AUTHORS O'Hara,P.J.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (01-APR-1992) Patrick J. O'Hara, ZymoGenetics, Inc.,
Seattle, WA 98105, USA
COMMENT Original source text: Rattus norvegicus cDNA to mRNA.
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ORIGIN

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Query Match: 98.18% Indels: 53
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US-10-828-332-7 (1-584) x RATMGLUR4A (1-4488)

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Qy 29 ArgArgAsnIleTrrPheAlaGluPheTrpGluAspAsnPheHisCysLysLeuSerArg 48
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 DEFINITION
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 VERSION BC072635.1 GI:49257159
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 4425)

REFERENCE
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Schetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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 Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 4425)
 Direct Submission
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
 Thomas L. Casavant
 Web site: http://genome.uiowa.edu
 Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
 Ronaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
 Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
 Scheetz, T., Smith, C., Snit, E., Tack, D., Trout, K., Walters, J.,
 Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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REMARK
 COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
 Thomas L. Casavant
 Web site: http://genome.uiowa.edu
 Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
 Ronaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
 Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
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ACCESSION AR149574
VERSION AR149574.1 GI:15114165
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2736)
AUTHORS Flor,P.Josef., Kuhn,R., Lindauer,K., Puttner,I. and Knopfel,T.
TITLE Human metabotropic glutamate receptor subtypes (hmr4, hmr6, hmr7)
JOURNAL Patent: US 6228610-A 1 08-MAY-2001;
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ORIGIN

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 DB 1468 AAGGTCATTGGCTCTGGAAGTACCACTGACCACTGACCTTAGAATAGCGGATGACCTGGCG 1527
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 DEFINITION A43637
 ACCESSION A43637.1 GI:2298839
 VERSION
 KEYWORDS
 SOURCE unidentified
 ORGANISM
 unclassified.
 1 (bases 1 to 2738)
 REFERENCE
 AUTHORS Flor, P. J., Kuhn, R., Lindauer, K., Puettner, I., and Knoepfel, T.
 TITLE HUMAN METABOTROPIC GLUTAMATE RECEPTOR SUBTYPES (HMR4, HMR6, HMR7)
 JOURNAL AND RELATED DNA COMPOUNDS
 COMMENT Patent: WO 9508627-A 1 30-MAR-1995;
 CIBA GEIGY AG (CH)
 Other publication CA 2171206 950330
 Other publication NO 961115 960319
 Other publication FI 961251 960318
 Other publication AU 7615994 950410.
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ORIGIN

Alignment Scores:

Pred. No.: 2,21e-242 Length: 2738
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Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 6 Gaps: 1

US-10-828-332-7 (1-584) x A43637 (1-2738)

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Db	1048	AGCCGACGCTGGACAAACACCGCGCAACATCTGGTTTCCGAGTTCGSGAGGACAA	1107
Qy	42	PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr	61
Db	1108	TTCCACTCAAGCTGAGCGCGCACGCCCTCAAGAAGGGCAGCCACGTCAGAGTGCACC	1167
Qy	62	AsnArgGluArgIleGlyClnAspSerAlaTyrGluGlnGluGlyValGlnPheVal	81
Db	1168	AACCGTAGCGAAATGGGCAGGATTCAGCTTATGAGCAGGAGGGGAGGTCAGTTTGTG	1227
Qy	82	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	101
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Qy	102	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr	121
Db	1288	GGCCGCGTGGGGCTCTGCCCGCATGCACCTGTAGATGGCACCCACGCTGTTAAGTAC	1347
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Db	1348	ATCCGAAACGTCAACTCTCAGGCATCCAGGGAAACCTGTGACCTTCATGAGAAATGGA	1407
Qy	142	AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr	161
Db	1408	GATGGCCTGGGGCTATGACATCTACCAATACCAGCTGCGCAACGATTCCTGCCGAGTAC	1467
Qy	162	LysValIleGlySerTrpThrAspHisIleuHisLeuArgIleGluArgMetGlnTrpPro	181
Db	1468	AAGGTCAATTGGCTCTCGACTGACCACCTGCACCTTAGAATAGACGGATGCACCTGGCCG	1527
Qy	182	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	201
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RESULT 7

Qy	242	ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal	261
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Db	1768	CTGCCCCCTCTCTCGCGGTGGTGGGATCGCTGCCACGTTGTTGTTGGTGGTGCATCACCTTT	1827
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Qy	342	LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer	361
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Qy	402	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer	421
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Qy	522	GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet	541
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Qy	542	SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu	561
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ACCESSION     AX427263
VERSION       AX427263.1 GI:21530616
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1
AUTHORS       Flor,P.J., Kuhn,R., Lindauer,K., Puettner,I. and Knoepfel,T.
TITLE         Human metabotropic glutamate receptor subtypes (hmr4, hmr6, hmr7)
JOURNAL       Patent: EP 1199359-A 1 24-APR-2002;
              Novartis AG (CH)
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Percent Similarity: 97.77%      Conservative: 6
Best Local Similarity: 96.74%    Mismatches: 12
Query Match:    96.70%          Indels:     1
DB:             6              Gaps:       1

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ACCESSION AKI22982
VERSION AKI22982.1 GI:34528429
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
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Negase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
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TITLE
JOURNAL
PUBMED

REFERENCE
AUTHORS

2 Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hiraoka, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuna, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project

TITLE
JOURNAL
REFERENCE
AUTHORS
TITILE
JOURNAL

3 (bases 1 to 3176)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
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DEFINITION Sequence 1 from patent US 6384205.
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VERSION AR208972.1 GI:21510266
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3431)
AUTHORS Belagaje,R.M. and Wu,S.
TITLE Metabotropic glutamate receptor 4 nucleic acid
JOURNAL Patent: US 6384205-A 1 07-MAY-2002;
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ORIGIN

Alignment Scores:
Pred. No.: 2,99e-242 Length: 3431
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: Gaps: 1

US-10-828-332-7 (1-584) x AR208972 (1-3431)

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VERSION AR208973.1 GI:21510267
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ORGANISM Unclassified.
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AUTHORS Belagaje,R.M. and Wu,S.
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JOURNAL Patent: US 6384205-A 3 07-MAY-2002;
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RESULT 11
HSU92457 3431 bp mRNA linear PRI 07-JUL-1999
LOCUS Human metabotropic glutamate receptor 4 mRNA, complete cds.
DEFINITION U92457
ACCESSION U92457
VERSION U92457.1 GI:1935038
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3431)
AUTHORS Wu, S., Wright, R.A., Rockey, P.K., Burgett, S.G., Arnold, J.S.,
Rostek, P.R. Jr., Johnson, B.G., Schoepf, D.D. and Belagaje, R.M.
TITLE Group III human metabotropic glutamate receptors 4, 7 and 8:
molecular cloning, functional expression, and comparison of
pharmacological properties in RGT cells
JOURNAL Brain Res. Mol. Brain Res. 53 (1-2), 88-97 (1998)
MEDLINE 98141892
PUBMED 9473604
REFERENCE 2 (bases 1 to 3431)
AUTHORS Wu, S. and Belagaje, R.M.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-1997) mc625, Eli Lilly and Company, Lilly
Corporate Center, Indianapolis, IN 46285, USA
FEATURES
source
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ORIGIN

Alignment Scores:

Pred. No.: 2, 99e-242 Length: 3431
Score: 3004.50 Matches: 564
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Best Local Similarity: 96.74% Mismatches: 12
Query Match: 96.70% Indels: 1
DB: 9 Gaps: 1

US-10-828-332-7 (1-584) x HSU92457 (1-3431)

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Qy	22	SerArgThrLeuAspAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn	41
Db	1073	AGCCGACGCTGGACAAACACCGGCGCAACATCTGTTTGGCGAGTTCTGGGAGGACAA	1132
Qy	42	PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysCysThr	61
Db	1133	TTCCACTGCAAGCTGAGCGCGCCACCGCTCAAGAGGGCAGCCACGTCAGAAAGTGAC	1192
Qy	62	AsnArgGluArgIleGlyGlnAspSerAlaTrpGluGlnGluGlyValGlnPheVal	81
Db	1193	AACCTGAGCGGAATTTGGGAGGATTCAGCTATGACGAGGAGGGGAAGGTGCGATTGTG	1252
Qy	82	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	101
Db	1253	ATCGATGCGGTGACGCCATGGGCCACGCGCTGCACGCCATGCACCGTACTGTGTCC	1312
Qy	102	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr	121
Db	1313	GGCCGCGTGGGGCTCTGCGCGCGCATGGACCCCTGTAGATGGCACCAGCTGCTTAAGTAC	1372
Qy	122	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	141
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Qy	142	AspAlaProGlyArgTyrAspIleTyrGlnLeuArgAsnGlySerAlaGluTyr	161
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Qy	162	LysValIleGlySerTrpThrAspHisIleuHisLeuArgIleGluArgMetGlnTrpPro	181
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Qy	182	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	201
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Qy	202	LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln	221
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Qy	222	TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn	241
Db	1673	TACCAAGTGGACCGCTACACCTGTAAAGACGTGTCCCTATGACATGCGGCCCCACAGAAAC	1732
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Qy	262	LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe	281

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Qy	362	AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu	381
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Qy	502	AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro	521
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RESULT 12

AK122836

LOCUS

DEFINITION Homo sapiens cDNA FLJ16445 fis, clone BRAMY3008937, highly similar to Metabotropic glutamate receptor 4 precursor.

ACCESSION AK122836

3850 bp mRNA linear

PRI 30-JAN-2004

AK122836.1	GI:34528033	
Oligo capping; fis (full insert sequence).		
ORGANISM		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,		
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Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S.		
Complete sequencing and characterization of 21,243 full-length		
human cDNAs		
Nat. Genet. 36 (1), 40-45 (2004)		
14702039		
2		
Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,		
Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R.,		
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Wagatsuma, M., Murakami, K., Kanehori, K., Sugiyama, A., Kawakami, B.,		
Suzuki, Y., Sugano, S., Negahari, K., Masuho, Y., Nagai, K. and		
Isogai, T.		
NEDO human cDNA sequencing project		
Unpublished		
3 (bases 1 to 3850)		
Isogai, T. and Yamamoto, J.		
Direct Submission		
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7		
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan		
(E-mail: genomics@ri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)		
NEDO human cDNA sequencing project supported by Ministry of		
Economy, Trade and Industry of Japan; cDNA full insert sequencing:		
Research Association for Biotechnology (RAB); cDNA library		
construction: Helix Research Institute (HRI) (supported by Japan		
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,		
HRI, and Biotechnology Center, National Institute of Technology and		
Evaluation; clone selection for full insert sequencing: HRI and		
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AR270511
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DEFINITION Sequence 1074 from patent US 6500938.
ACCESSION AR270511
VERSION AR270511.1 GI:29701745
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3884)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1074 31-DEC-2002;
FEATURES
LOCATION/Qualifiers
source 1..3884
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ORIGIN
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Db 1338 AACCTGAGCCAAATGGCAGGATTCAGCTTATGACGAGGAGGGGAAAGTGCAGTTGTG 1397
Qy 82 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
Db 1398 ATCATGTCGTGTACGCCATGGCCACGCGCTGACCGCATGACCGTACCGTGTGTGCC 1457
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Qy      182  |||||GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGluArg 201
Db      1698  |||||GGGACGGGGCAGCAGCTGCCCGCTCCATCTGCAGCCTGCCCTGCCAACCGGGTGAGCGG 1757
Qy      202  |||||LysLysThrValLysGlyMetAlaCysCysStrHisCysGluProCysThrGlyTyrGln 221
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Qy      242  |||||ArgThrSerCysGlnProIleValLysLeuGluTrpAspSerProTrpAlaVal 261
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Qy      422  |||||LeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuMetValThrCysThrVal 441
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DEFINITION Sequence 14 from patent US 6608176.
ACCESSION  AR381464
VERSION     AR381464.1  GI:40089522
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 3884)
AUTHORS    Chaudhari, N. and Roper, S.D.
TITLE       Taste receptor for umami (monosodium glutamate) taste
JOURNAL     Patent: US 6608176-A 14 19-AUG-2003;
FEATURES    Location/Qualifiers
             source          1..3884
             /organism="unknown"
             /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:      3,53e-242      Length:      3884
Score:          3004.50        Matches:     564
Percent Similarity: 97.77%      Conservative: 6
Best Local Similarity: 96.74%    Mismatches: 12
Query Match:    96.70%         Indels:      1
DB:             6              Gaps:        1

US-10-828-332-7 (1-584) x AR381464 (1-3884)
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Db      1158  |||||GGTCTGTACGATCTCTCCCAAGAGGATGTCCGTACGAGGCTTCGACCGCTACTTCTCC 1217
Qy      22  SerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 41
Db      1218  |||||AGCCGCACGTGGCAACAACACCGCGCAACATCTGTGTTGCCGAGTTCTGGGAGGACAAC 1277
Qy      42  PheHisCysLysLeuSerArgHisAlaLeuLysGlySerHisIleLysLysCysThr 61
Db      1278  |||||TTCACCTGCAAGCTGAGCCGCCACGCCCTCAAGAAGGGCAGCCACGTCAGAAGTGCACC 1337
Qy      62  AsnArgGluArgIleGlyGlnAspSerAlaTyrGlnGluGlyLysValGlnPheVal 81
Db      1338  |||||AACCGTGAGCGAATTGGCGAGGATTCAGCTTATGAGCAGGAGGGGAGGTGACGTTGTG 1397
Qy      82  IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 101
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Qy      102  GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 121
Db      1458  |||||GGCCCGGTGGGGTCTCTCCCGCGCATGGACCTGTAGATGGCACCCAGCTGCTTAAGTAC 1517
Qy      122  IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 141
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Db 1638 AAGGTCAATGGCTCTCGGACTGACCACTGCACCTTAGAATAGAGCGGATGCACTGGCGG 1697
QY 182 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 201
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Db 2418 GACCTGTCTGCTATCTGCTGCTGGGCTACAGCATGCTCTCATGGTCACTGCGCACCGGTG 2477
QY 442 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 461
Db 2478 TATGCCATCAAGACCGCGGTGCCCGAGACTTCAATGAGGCCAAGCCCATTTGGCTTC 2537
QY 462 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 481
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QY 482 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 501

Db 2598 CAGTCGGCGGCAACGCTGTACATCCAGAGCAGCGCTGACCGTCTCGGTGAGTCTGAGC 2657
QY 502 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 521
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QY 582 HisAlaIle 584
Db 2898 CATGCAATC 2906

Search completed: June 21, 2005, 14:17:50
Job time : 7366 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 17:59:49 ; Search time 178 Seconds
(without alignments)
1680.080 Million cell updates/sec

Title: US-10-828-332-7
Perfect score: 3107
Sequence: 1 MGVSSSLPTMTSGFDYF.....LETPALATKQTYVVTNHAI 584

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3004.5	96.7	912	1 MGR4 HUMAN	Q14833 homo sapien
3	2720.5	87.6	983	2 Q62916	Q62916 rattus norv
4	2719	87.5	796	2 Q62MQ2	Q62mq2 homo sapien
5	2546.5	82.0	832	2 Q68EF4	Q68ef4 mus musculu
6	2377	76.5	908	1 MGR8 HUMAN	Q08222 homo sapien
7	2377	76.5	908	2 Q6B964	Q6B964 mus musculu
8	2371	76.3	908	1 MGR8 RAT	P70579 rattus norv
9	2336	75.2	908	1 MGR8 MOUSE	P47743 mus musculu
10	2219	71.4	915	1 MGR7 HUMAN	Q14831 homo sapien
11	2214	71.3	915	2 Q68ED2	Q68ed2 mus musculu
12	2210	71.1	915	1 MGR7 RAT	P35400 rattus norv
13	2189	70.5	906	2 Q8NFS2	Q8nfs2 homo sapien
14	2189	70.5	911	2 Q8NFS3	Q8nfs3 homo sapien
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18	2052.5	66.1	877	1 MGR6 HUMAN	Q15303 homo sapien
19	2044	65.8	868	2 Q863I4	Q863i4 oryctolagus
20	2025	65.2	871	1 MGR6 RAT	P35349 rattus norv
21	1967.5	63.3	546	2 Q8CFQ7	Q8cfq7 mus musculu
22	1855	59.7	620	2 Q76E43	Q76e43 poephila gu
23	1813	58.4	977	2 Q9PWE1	Q9pwe1 ictalurus p
24	1284.5	41.3	1520	2 Q8NHA9	Q8nha9 homo sapien
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27	1223.5	39.4	1073	2 Q7OGQ8	Q7ogq8 drosophila
28	1223.5	39.4	1226	2 Q9V4U3	Q9v4u3 drosophila
29	1223.5	39.4	1264	2 Q9V4U4	Q9v4u4 drosophila
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31	1179	37.9	843	2 Q6S738	Q6s738 apis mellif

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34	1155.5	37.2	879	1 MGR3 MOUSE	Q9gye2 mus musculu
35	1155.5	37.2	879	2 Q86YG6	Q86yg6 homo sapien
36	1152.5	37.1	879	1 MGR3 RAT	P31422 rattus norv
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ALIGNMENTS

RESULT 1

ID MGR4 RAT STANDARD; PRT; 912 AA.
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DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 4 precursor (mGluR4).
GN Name=Grm4; Synonyms=Gprcld, Mglur4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
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RC TISSUE=Brain;
RX MEDLINE=921110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93334699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thøgersen H., Venezia D., Haldeman B.A., McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
RN [3]
RP INTERACTION WITH PRKCAPB.
RX MEDLINE=20571397; PubMed=1122333;
RA El Far O., Airas J., Wischmeyer E., Nehring R.B., Karschin A., Betz H.;
RT "Interaction of the C-terminal tail region of the metabotropic glutamate receptor 7 with the protein kinase C substrate PICK1.";
RL Eur. J. Neurosci. 12:4215-4221(2000).
CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is mediated by a G-protein that inhibits adenylate cyclase activity.
CC -!- SUBUNIT: Interacts with PRKCAPB.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Is widely distributed in the CNS. Predominant expression is seen in the granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M92077; -; NOT_ANNOTATED_CDS.

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DR EMBL; M90518; AAA93190.1; -.
DR PIR; JH0563; JH0563.
DR HSSP; P23385; 1EWK.
DR RGD; 2745; Gm4.
DR InterPro; IPR001028; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001162; Mglu_receptor.
DR InterPro; IPR001786; Mglu_receptor4.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family; Signal;
Transmembrane.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 912 Metabotropic glutamate receptor 4.
FT DOMAIN 33 587 Extracellular (Potential).
FT TRANSMEM 588 610 1 (Potential).
FT DOMAIN 611 624 Cytoplasmic (Potential).
FT TRANSMEM 625 645 2 (Potential).
FT DOMAIN 646 656 Extracellular (Potential).
FT TRANSMEM 657 675 3 (Potential).
FT DOMAIN 676 699 Cytoplasmic (Potential).
FT TRANSMEM 700 720 4 (Potential).
FT DOMAIN 721 750 Extracellular (Potential).
FT TRANSMEM 751 772 5 (Potential).
FT DOMAIN 773 785 Cytoplasmic (Potential).
FT TRANSMEM 786 808 6 (Potential).
FT DOMAIN 809 821 Extracellular (Potential).
FT TRANSMEM 822 847 7 (Potential).
FT DOMAIN 848 912 Cytoplasmic (Potential).
FT CARBOHYD 98 98 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 301 301 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 454 454 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 484 484 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 569 569 N-linked (GlcNAc... ) (Potential).
FT CONFLICT 124 124 Q -> R (in Ref. 2).
SQ SEQUENCE 912 AA; 101818 MW; 336430EF19B4B577 CRC64;

Query Match
Best Local Similarity 98.2%; Score 3050.5; DB 1; Length 912;
Matches 575; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 3 GVSSSLPRMT-SGPDYFSSRTLDNRRNIWFAEFWEDNFCHKLSRHALKKGSHIKKCT 61
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QY 62 NRERTGDSAYEKGKQVFDVAVYMGHALHMRDLCPRGVGICPRMDPVDGTQLLY 121
DB 390 NRERTGDSAYEKGKQVFDVAVYMGHALHMRDLCPRGVGICPRMDPVDGTQLLY 449
QY 122 IRNVNFSIAGNPVTFFNENGDPAGRYDIYQYQLRNGSAEYKIVGSWTDLHLRIERMQWP 181
DB 450 IRNVNFSIAGNPVTFFNENGDPAGRYDIYQYQLRNGSAEYKIVGSWTDLHLRIERMQWP 509
QY 182 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQYQVDRYTKCTCPYDMRPTE 241
DB 510 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQYQVDRYTKCTCPYDMRPTE 569
QY 242 RTSQOPIPIVLEWDSPAVLPFLAVVGIATLFWVVTFFRYNDPTIVKASGRELVSVL 301
DB 570 RTSQOPIPIVLEWDSPAVLPFLAVVGIATLFWVVTFFRYNDPTIVKASGRELVSVL 629
QY 302 LAGIFLCVATYFLMAEPDLGTCSLRIFFLGLGMSISYAALLTKNRIYRIFEQGKRSVS 361
DB 630 LAGIFLCVATYFLMAEPDLGTCSLRIFFLGLGMSISYAALLTKNRIYRIFEQGKRSVS 689
QY 362 APRFTSPASQAITPILISLQLLGICVWFVVDPPSHVVDFOQRTLDPRFARGVLKCDIS 421
DB 690 APRFTSPASQAITPILISLQLLGICVWFVVDPPSHVVDFOQRTLDPRFARGVLKCDIS 749

```

RESULT 2

MGR4_HUMAN

ID_MGR4_HUMAN

AC Q14833;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Metabotropic glutamate receptor 4 precursor (mGluR4).

GN Name=GRM4; Synonyms=GPRC1D, MGLUR4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=96346635; PubMed=8738157; DOI=10.1016/0169-328X(95)00321-1;

RA Makoff A., Lelchuk R., Oxer M., Harrington K., Emson P.;

RT "Molecular characterization and localization of human metabotropic

RT glutamate receptor type 4.";

RL Brain Res. Mol. Brain Res. 37:239-248(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98141892; PubMed=9473604; DOI=10.1016/S0169-328X(97)00277-5;

RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,

RA Rostek P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;

RT "Group III human metabotropic glutamate receptors 4, 7 and 8:

RT molecular cloning, functional expression, and comparison of

RT pharmacological properties in RGT cells.";

RL Brain Res. Mol. Brain Res. 53:88-97(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=95342351; PubMed=7617140; DOI=10.1016/0028-3908(94)00149-M;

RA Flor P.J., Lukic S., Rueegg D., Leonhardt T., Knoepfel T., Kuhn R.;

RT "Molecular cloning, functional expression and pharmacological

RT characterization of the human metabotropic glutamate receptor type

RT 4.";

RL Neuropharmacology 34:149-155(1995).

RN [4]

RP VARIANT ILE-797.

RX MEDLINE=21416233; PubMed=11525421;

RA Ohtsuki T., Toru M., Arinami T.;

RT "Mutation screening of the metabotropic glutamate receptor mGluR4

RT (GRM4) gene in patients with schizophrenia.";

RL Psychiatr. Genet. 11:79-83(2001).

CC -1- FUNCTION: Receptor for glutamate. The activity of this receptor is

CC mediated by a G-protein that inhibits adenylate cyclase activity.

CC -1- SUBUNIT: Interacts with PRKCAIP (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Strongly expressed in the cerebellum.

CC No expression detected in liver.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to a license@isb-sib.ch)

EMBL; X80818; CAA56784.1; -;
EMBL; U92457; AAB51762.1; -;
HSP; P23385; LEWK.
Genew; HGNC:4596; GRM4.
MIM; 604100; -;
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . ; TAS.
GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . ; TAS.
GO; GO:0007268; P:synaptic transmission; TAS.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
InterPro; IPR000162; Mglu_receptor.
InterPro; IPR001786; Mglu_receptor4.
Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
G-protein coupled receptor; Glycoprotein; Multigene family;
Polymorphism; Signal; Transmembrane.

SIGNAL 1 32 Potential.
FT CHAIN 33 912 Metabotropic glutamate receptor 4.
FT DOMAIN 33 587 Extracellular (Potential).
FT TRANSMEM 588 610 1 (Potential).
FT DOMAIN 611 624 Cytoplasmic (Potential).
FT TRANSMEM 625 645 2 (Potential).
FT DOMAIN 646 656 Extracellular (Potential).
FT TRANSMEM 657 675 3 (Potential).
FT DOMAIN 676 699 Cytoplasmic (Potential).
FT TRANSMEM 700 720 4 (Potential).
FT DOMAIN 721 750 Extracellular (Potential).
FT TRANSMEM 751 772 5 (Potential).
FT DOMAIN 773 785 Cytoplasmic (Potential).
FT TRANSMEM 786 808 6 (Potential).
FT DOMAIN 809 821 Extracellular (Potential).
FT TRANSMEM 822 847 7 (Potential).
FT DOMAIN 848 912 Cytoplasmic (Potential).
FT CARBOHYD 98 98 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 301 301 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 454 454 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 484 484 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 569 569 N-linked (GlcNAc. .) (Potential).
FT VARIANT 797 797 V -> I.
FT SIGNAL 912 AA; 101867 MW; 4A2F3E63A2BAFA5A CRC64;
/FTId=VAR_012992.

SEQUENCE 912 AA; 101867 MW; 4A2F3E63A2BAFA5A CRC64;
Query Match 96.7%; Score 3004.5; DB 1; Length 912;
Best Local Similarity 96.7%; Pred. No. 1.7e-236;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 3 GVSSSLPTMT-SGFDRYFSSRTLNNRRNIWFAEFWDNFHCKLSRHALKKGSHIKCT 61
DB 330 GAVTILPKMSVRGDFRYFSSRTLNNRRNIWFAEFWDNFHCKLSRHALKKGSHVKKCT 389
QY 62 NRERICQDSAYEGKGVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLKY 121
DB 390 NRERICQDSAYEGKGVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLKY 449
QY 122 IRWNFSGIAGNPVTNENGDPGRDYIYOQLRNGSAEYKIVGSWTDLHLRIERMQWP 181
DB 450 IRWNFSGIAGNPVTNENGDPGRDYIYOQLRNGSAEYKIVGSWTDLHLRIERMEHP 509
QY 182 GSGQQLPRLSCPLPCPGGRKKTVMGMA CWMCCEPCTGYOQVDRYTCTCYDMRPRTEN 241
DB 510 GSGQQLPRLSCPLPCPGGRKKTVMGMP CWMCCEPCTGYOQVDRYTCTCYDMRPRTEN 569
QY 242 RTSCQPIPIVKLEWDSFWAVLPLFLAVVGIAATLFVVITFVRYNDTPIVKASGRELSYVL 301

Db 570 RTGCRPIPIVKLEWDSFWAVLPLFLAVVGIAATLFVVITFVRYNDTPIVKASGRELSYVL 629
QY 302 LAGIFLCYATTFTLMIAEPDLGTCSLARRIFLGKMSISYAALTTKTNRIYRIPEQGRSRVS 361
Db 630 LAGIFLCYATTFTLMIAEPDLGTCSLARRIFLGKMSISYAALTTKTNRIYRIPEQGRSRVS 689
QY 362 APRFISPASQAIFTILISLQLLIGICWFVVPDPSHSVDFQDQRTLDPRFARGVLKCDIS 421
Db 690 APRFISPASQAIFTILISLQLLIGICWFVVPDPSHSVDFQDQRTLDPRFARGVLKCDIS 749
QY 422 DLSLICLLGYSMLLMWTCTTYAIKTRGVPTNEAKPIGFTWTTTCIWLARIPPECTS 481
Db 750 DLSLICLLGYSMLLMWTCTTYAIKTRGVPTNEAKPIGFTWTTTCIWLARIPPECTS 809
QY 482 QSDADKLVIQTTLTVSVLSASVSLGMYPMKVYIILFHPEQNVPRKRSLKAVTAATM 541
Db 810 QSDADKLVIQTTLTVSVLSASVSLGMYPMKVYIILFHPEQNVPRKRSLKAVTAATM 869
QY 542 SNRKFTQGNFRPNGEAKSELCELNETPALATKQTVYVYTNHAI 584
Db 870 SNRKFTQGNFRPNGEAKSELCELNETPALATKQTVYVYTNHAI 912

RESULT 3
Q62916 PRELIMINARY; PRT; 983 AA.
AC Q62916; 06-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Metabotropic glutamate receptor 4b.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_taxid=10116;
RX (1)
RP SEQUENCE FROM N.A.
RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47331; AAA89788.1; -.
DR HSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mglu_receptor.
DR InterPro; IPR001786; Mglu_receptor4.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMGR.
DR PRINTS; PR01054; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 983 AA; 109276 MW; 072FD8B3A840A80 CRC64;
Query Match 87.6%; Score 2720.5; DB 2; Length 983;
Best Local Similarity 98.5%; Pred. No. 2.9e-213;
Matches 511; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 3 GVSSSLPTMT-SGFDRYFSSRTLNNRRNIWFAEFWDNFHCKLSRHALKKGSHIKCT 61
DB 330 GAVTILPKMSVRGDFRYFSSRTLNNRRNIWFAEFWDNFHCKLSRHALKKGSHIKCT 389
QY 62 NRERICQDSAYEGKGVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLKY 121

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Db 390 NRERIGQDSAYEQGKVQFVIDAVYAMGHAMHRLDCPRGVLCPRMDPVDGTQLLKY 449
Qy 122 IRNVNFSGIAGNPVTNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIERQWP 181
Db 450 IRNVNFSGIAGNPVTNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIERQWP 509
Qy 182 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQVDRYTCCTCPYDMRPTE 241
Db 510 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQVDRYTCCTCPYDMRPTE 569
Qy 242 RTSCQPIPIVKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTSCQPIPIVKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 629
Qy 302 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 361
Db 630 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 689
Qy 362 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db 690 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 481
Db 750 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 809
Qy 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFPH 520
Db 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFPH 848

RESULT 4
Q62MQ2
ID Q62MQ2 PRELIMINARY; PRT; 796 AA.
AC Q62MQ2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16766.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuna M., Murakawa K., Kanehori K., Takahashi-Pujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131536; BAD18673.1; -.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0008067; F.metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR GO; GO:0004872; E.receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mrglu_receptor.
DR InterPro; IPR001786; Mrglu_receptor4.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMRG.
DR PRINTS; PR01054; MTABOTROPIC4R.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00980; G_PROTEIN_RECF_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECF_F3_3; 1.
DR PROSITE; PS00981; G_PROTEIN_RECF_F3_4; 1.
DR PROSITE; PS00981; G_PROTEIN_RECF_F3_4; 1.
KW Receptor.
SQ SEQUENCE 796 AA; 88492 MW; FAB466D1D45D3829 CRC64;
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Query Match 87.5%; Score 2719; DB 2; Length 796;

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Best Local Similarity 97.9%; Pred. No. 3e-213;
Matches 512; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 62 NRERIGQDSAYEQGKVQFVIDAVYAMGHAMHRLDCPRGVLCPRMDPVDGTQLLKY 121
Db 274 DRERIGQDSAYEQGKVQFVIDAVYAMGHAMHRLDCPRGVLCPRMDPVDGTQLLKY 333
Qy 122 IRNVNFSGIAGNPVTNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIERQWP 181
Db 334 IRNVNFSGIAGNPVTNENGDAPEGYDIYQVLRNGSAEYKVIQSWTDHLHLRIERQWP 393
Qy 182 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQVDRYTCCTCPYDMRPTE 241
Db 394 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQVDRYTCCTCPYDMRPTE 453
Qy 242 RTSCQPIPIVKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 301
Db 454 RTGCRPIPIIKLEWDSPAWVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYVL 513
Qy 302 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 361
Db 514 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 573
Qy 362 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db 574 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 633
Qy 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 481
Db 634 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIIVLAFIPIFFGTS 693
Qy 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFPH 520
Db 694 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFPH 753
Qy 542 SNKFTQGNFRPNGEAKSELLENLEPALATKQYVYVYTNHAI 584
Db 754 SNKFTQGNFRPNGEAKSELLENLEPALATKQYVYVYTNHAI 796

RESULT 5
Q68EF4
ID Q68EF4 PRELIMINARY; PRT; 832 AA.
AC Q68EF4;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
```


QY 302 LAGIFLCYATTFLMTAEBDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 361
 DB 626 LTGIFLCYSITFLMIAADPTTICSPRRIFLGLGMCFSYAALLTKNRIHRIFEQKKSVT 685
 QY 362 APRFISPASQALITFILISLQLLGICGVFWVVDPPSHSVDFDQRTLDPRFARGVLKCDIS 421
 DB 686 APKFISPASQALVITFSLISVQLLGCVFWVVDPPHTIIDYGEQRTLDPENARGVLKCDIS 745
 QY 422 DLSLICLLGYSMLLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTS 481
 DB 746 DLSLICLSGYSILLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTA 805
 QY 482 QSAKLYIQTTTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 541
 DB 806 QSAEKMYIQTTTTLTVSMLSASVSLGMLYMPKVYIILFHPQONVQKRSKPAVVTAATM 865
 QY 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVTYTHAI 584
 DB 866 QSKLIQKGNDRPNGEVKSSELCELETNTSSTKTYIISYNSHSI 908
 RESULT 9
 ID MGR8 MOUSE STANDARD; PRT; 908 AA.
 AC P47743;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Metabotropic glutamate receptor 8 precursor (mGluR8).
 GN Name=Gm8; Synonyms=Gprclh, mGluR8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Retina;
 RX MEDLINE=95239344; PubMed=7722846;
 RA Duvoisin R.M., Zhang C., Ramonell K.;
 RT "A novel metabotropic glutamate receptor expressed in the retina and
 RT olfactory bulb";
 RL J. Neurosci. 15:3075-3083(1995).
 CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is
 CC mediated by a G-protein that inhibits adenylyate cyclase activity.
 CC -!- SUBUNIT: Interacts with PKRCAP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Strongly expressed in olfactory bulb,
 CC accessory olfactory bulb, and mammillary body. Weaker expression
 CC in the retina, and in scattered cells in the cortex and hindbrain.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U17252; AAA68149.1; -;
 DR PIR; I49142; I49142.
 DR HSP; P23385; LEWK.
 DR MGD; MGI:1351345; Gm8.
 DR GO; GO:0001642; F:group III metabotropic glutamate receptor a. . .; IDA.
 DR InterPro; IPRO01828; ANF receptor.
 DR InterPro; IPRO00337; GPCR_Mgr.
 DR InterPro; IPRO00162; Metglu_receptor.
 DR InterPro; IPRO00144; Metglu_receptor8.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 KW G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
 KW Signal; Transmembrane.
 FT SIGNAL 1 33 Potential.
 FT CHAIN 34 908 Metabotropic glutamate receptor 8.
 FT DOMAIN 34 583 Extracellular (Potential).
 FT TRANSMEM 584 608 1 (Potential).
 FT DOMAIN 609 620 Cytoplasmic (Potential).
 FT TRANSMEM 621 641 2 (Potential).
 FT DOMAIN 642 647 Extracellular (Potential).
 FT TRANSMEM 648 668 3 (Potential).
 FT DOMAIN 669 695 Cytoplasmic (Potential).
 FT TRANSMEM 696 716 4 (Potential).
 FT DOMAIN 717 746 Extracellular (Potential).
 FT TRANSMEM 747 768 5 (Potential).
 FT DOMAIN 769 781 Cytoplasmic (Potential).
 FT TRANSMEM 802 803 6 (Potential).
 FT DOMAIN 804 818 Extracellular (Potential).
 FT TRANSMEM 819 843 7 (Potential).
 FT DOMAIN 844 908 Cytoplasmic (Potential).
 FT CARBOHYD 95 95 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 298 298 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 452 452 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 480 480 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 565 565 N-linked (GlcNAc. .) (Potential).
 SQ SEQUENCE 908 AA; 101413 MW; 4CDD9D35827ED41F CRC64;
 Query Match 75.2%; Score 2336; DB 1; Length 908;
 Best Local Similarity 74.1%; Pred. No. 7,1e-182;
 Matches 432; Conservative 60; Mismatches 89; Indels 2; Gaps 2;
 QY 3 GVSSSLPRTWT-SGFDYRFSRSLDNNRNINWFAEFWEDNFHCKLSRHALKGSHIKKCT 61
 DB 327 GAVTILPKRASIDGDFRFSRSLTANNRRNVWFAEFSEGNFGCKSGSHG-KRNSHIKCT 385
 QY 62 NRERIGODSAVEQSGKQVFDIVAYMGHALHAMHRLDCPRVGLCPRMDPDVDTQLKY 121
 DB 386 GLERKADSSYEQKGKQVFDIVAYSMAYALHNMHKLCPGYIGLCPRMTIDKELLGY 445
 QY 122 IRNVNFSGIAGNPVTNENGADPGRYDIYQQLRNGSAEYKVIGSWTDHLHLRIERQWP 181
 DB 446 IRNVNFSAGTPTVTNENGADPGRYDIYQVQINNKSTEVKIIGHWTNQLHLKVEDMQWA 505
 QY 182 GSGQLPRSTCLSPQGBERKTKVGMACWHCEPCTGYQVDRYTKCTCPYDMRPTEN 241
 DB 506 NREHTHPASVCSLPCKPGERKTKVGPCCWHCGCEGYNQVDELSCCLPLDQRPNN 565
 QY 242 RTSCQPIPIVKLEWDSWAVLPLFVAVGIAATLVVVVTVRVYNDTPVKGASGRELSTVL 301
 DB 566 RTGQRIPITIKLEWHSWAVVPLIALGIATTVFVTVRVYNDTPVKGASGRELSTVL 625
 QY 302 LAGIFLCYATTFLMIAEBDLGTCSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVS 361
 DB 626 LTGIFLCYSITFLMIAADPTTICSPRRIFLGLGMCFSYAALLTKNRIHRIFEQKKSVT 685
 QY 362 APRFISPASQALITFILISLQLLGICGVFWVVDPPSHSVDFDQRTLDPRFARGVLKCDIS 421
 DB 686 APKFISPASQALVITFSLISVQLLGCVFWVVDPPHTIIDYGEQRTLDPENARGVLKCDIS 745
 QY 422 DLSLICLLGYSMLLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTS 481
 DB 746 DLSLICLSGYSILLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTA 805
 QY 482 QSAKLYIQTTTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 541
 DB 806 QSAEKMYIQTTTTLTVSMLSASVSLGMLYMPKVYIILFHPQONVQKRSKPAVVTAATM 865
 QY 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVTYTHAI 584
 DB 866 QSKLIQKGNDRPNGEVKSSELCELETNTSSTKTYIISYNSHSI 908

mediated by a G-protein that inhibits adenylate cyclase activity.

-1- SUBUNIT: Interacts with PRKCBP.

-2- SUBCELLULAR LOCATION: Integral membrane protein.

-3- TISSUE SPECIFICITY: Widely distributed throughout the brain.

-4- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.

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EMBL; D16817; BAA04092.1; -

EMBL; U06832; AAA20655.1; -

PIR; A49874; A49874.

HSSP; P23385; LEWK.

RGD; 619857; Gm7.

InterPro; IPR001828; ANF_receptor.

InterPro; IPR000337; GPCR_Mgr.

InterPro; IPR000162; Mtblu_receptor.

InterPro; IPR001883; Mtblu_receptor7.

Pfam; PF00003; 7tm_3; 1.

Pfam; PF01094; ANF_receptor; 1.

PRINTS; PR00248; GPCR_MGR.

ProSITE; PS00379; G_PROTEIN_RECEP_F3_1; 1.

ProSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.

ProSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

ProSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.

G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction; Signal; Transmembrane.

SIGNAL 1 32 Potential.

CHAIN 33 915 Metabotropic glutamate receptor 7.

DOMAIN 33 590 Extracellular (Potential).

TRANSMEM 591 615 1 (Potential).

DOMAIN 616 627 Cytoplasmic (Potential).

TRANSMEM 628 648 2 (Potential).

DOMAIN 649 654 Extracellular (Potential).

TRANSMEM 655 675 3 (Potential).

DOMAIN 676 702 Cytoplasmic (Potential).

TRANSMEM 703 723 4 (Potential).

DOMAIN 724 753 Extracellular (Potential).

TRANSMEM 754 775 5 (Potential).

DOMAIN 776 788 Cytoplasmic (Potential).

TRANSMEM 789 810 6 (Potential).

DOMAIN 811 825 Extracellular (Potential).

TRANSMEM 826 850 7 (Potential).

DOMAIN 851 915 Cytoplasmic (Potential).

CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).

CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).

CARBOHYD 486 486 N-linked (GlcNAc...) (Potential).

CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).

SEQUENCE 915 AA; 102231 MW; F28APC4G645A6C2 CRC64;

Query Match 71.1%; Score 2210; DB 1; Length 915;

Best Local Similarity 69.5%; Pred. No. 1.4e-171;

Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

QY 3 GVSSSLPRMT-SGDRYFSSRTLDNRRNTWFAEFWEDNFCKLSRLHKKGSHIKCT 61

DB 332 GAITIQKRAIVTEGDFYFTSRTLENNRRNVFAEYWEENFCKLTISGSKEDTDRKCT 391

QY 62 NRERIGDSAYEQEGKQVFVDVAVMGHALHMRDLCPGRVGLCPRMDPVDGTLQKY 121

DB 392 QGERIGKDSNTEQEGKQVFVDVAVMAHALHMRDLCPGRVGLCPRMDPVDGTLQKY 451

QY 122 IRNVNFSGIAGNVTFNENGDAPGRYDIYQQLRN-GSAEYKVGISWTDHLHLRIERMQW 180

DB 452 IRNVNFSGAGTPVWFNKGADPGRYDIYQQLRN-GSAEYKVGISWTDHLHLRIERMQW 511

QY 101 PGSGOOLPRSTCSLPCQGERKKTIVKGMACCMHCEPCTGYQVDRYTKCTCPYDMRTE 240

DB 452 IRNVNFSGAGTPVWFNKGADPGRYDIYQQLRN-GSAEYKVGISWTDHLHLRIERMQW 511

Db 512 KGKVEIPSSVCTLPCKPGQRKKTKGTGTPCCWTCBPDGYQVQFDEMTCQHCYPDORPNE 571

QY 241 NRTSQPIPIVKLEWDSFPAVLFLAVVGAATLFVVVTVFVRYNDTPIVKSAGRELSYV 300

DB 572 NRTGQNPILIKLEWHSFPAVLFLAVVGAATLFVVVTVFVRYNDTPIVKSAGRELSYV 631

QY 301 LLAGFLCYATFLMAEPDLGTCSLRIFPLGLGMSISYAAALLTKTNRIYRIFEQGRSV 360

DB 632 LLTGIFLCYITFLMAEPDLGTCSLRIFPLGLGMSISYAAALLTKTNRIYRIFEQGRSV 691

QY 361 SAPRFISAPOLATIFLLISLQLLIGICVWFVVDPSHVSVDFOFOTLDRPRARGVLKCDI 420

DB 692 TAPRLISFTSQAITSLSISVQLLGVFVFWGVDPPNIIIDYDEHKTMPQEQARGVLKCDI 751

QY 421 SDLSLICLLGYSMMLMVTCTVVAIKTRGVPEFNEAKPIGFTMTYTCIVWLAFIPFOT 480

DB 752 TDLQIICSLGYSIILLMVTCTVVAIKTRGVPEFNEAKPIGFTMTYTCIVWLAFIPFOT 811

QY 481 SOSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAAT 540

DB 812 AQSAEKLYIQTTTLTISNLSASVALGMLYMPKVYIILFHPQONVPRKRSKAVVTAAT 871

QY 541 MSNKFTQGNRPNGEAKSELCELETALATKOTVYVYTNHAI 584

DB 872 MSSRLSHKPSDRPNGEAKSELCELETALATKOTVYVYTNHAI 915

RESULT 13

Q8NFS2 PRELIMINARY; PRT; 906 AA.

ID Q8NFS2

AC Q8NFS2; 22, Created

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

GN Metabotropic glutamate receptor 7 variant 5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22048149; PubMed=12052533; DOI=10.1016/S0304-3940(02)00306-3;

RA Schulz H.L., Steohr H., Weber B.H.F.;

RT "Characterization of three novel isoforms of the metabotropic

RL glutamate receptor 7 (GRM7).";

DR Neurosci. Lett. 326:37-40(2002).

DR EMBL; AF458054; AA047559.1; -

DR HSSP; P23385; LEWK.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008057; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR001828; ANF_receptor.

DR InterPro; IPR000337; GPCR_Mgr.

DR InterPro; IPR000162; Mtblu_receptor.

DR InterPro; IPR001883; Mtblu_receptor7.

DR Pfam; PF00003; 7tm_3; 1.

DR Pfam; PF01094; ANF_receptor; 1.

DR Pfam; PF07562; NCD3G; 1.

DR PRINTS; PR00248; GPCR_MGR.

DR PRINTS; PR01057; MTABOTROPICR.

DR PRINTS; PR00593; MTABOTROPICR.

DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.

DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.

KW Receptor.

SQ SEQUENCE 906 AA; 101301 MW; 53EC7BB83CBCB61 CRC64;

Query Match 70.5%; Score 2189; DB 2; Length 906;

Best Local Similarity 70.8%; Pred. No. 7.3e-170;

Matches 401; Conservative 71; Mismatches 92; Indels 2; Gaps 2;

Job time : 182 secs

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RA Schulz H.L., Stoeck H., Weber B.H.F.;
RT "Characterization of three novel isoforms of the metabotropic
RL glutamate receptor 7 (GRM7)".
RL Neurosci. Lett. 326:37-40(2002).
DR EMBL; AF458052; AAM47557.1; -.
DR HSSP; P23385; 1EWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mglu_receptor.
DR InterPro; IPR001883; Mglu_receptor7.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR01057; MTABOTROPCTR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS02559; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 924 AA; 103375 MW; 32028B6156A71BFE CRC64;

Query Match 70.5%; Score 2189; DB 2; Length 924;
Best Local Similarity 70.8%; Pred. No. 7.4e-170;
Matches 401; Conservative 71; Mismatches 92; Indels 2; Gaps 2;

QY 3 GYSSSLPTMT-SGDFRYFSRSLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
DB 332 GAITTPKRAIVGEGFDAYFTSRITLNNRRNVFAEYWEENFNCKLTISGSKKEDTRKCT 391

QY 62 NHERIGDSAYQEGKVQVIVDAVYANGHALHAMHRDLCPGRVGLCPMDPVDGTQLLY 121
DB 392 GQERIGKDSNYEQGVQVIVDAVYAMAHALHHMKDLCADYRGVCPENEGAGGKLLKY 451

QY 122 IRNVNPSGIAGNPVTNENGDPGRYDIYQYQLRNGS-AEYKVIGSWTDHLHLRIERMOW 180
DB 452 IRNVNPSGAGTFVFNKNGDAPGRYDIYQYQTNTSNFGYRLIGQWTDQLNIEDMOW 511

QY 181 PGSGQQLPRISCSLPQCPGKERKTKVGMACCMHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
DB 512 GKGVRIPASVCTLPCKPGQRKTKGTCCWTCPCDGYQYQFDEMTQCHCPYDQRPNE 571

QY 241 NRTSQPIPIVLEWSPWAVLPFLAVVGIATLFFVVVTFVRYNDTPIVKASGRELSYV 300
DB 572 NRTGQDIPIIKLEWSPWAVIPVFLAMLGIIATIFVWATFIRYNDTPIVRASGRELSYV 631

QY 301 LLAGIFLCYATFLMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSV 360
DB 632 LITGIFLCYIIITFLMTAKPDVAVCSFRRVFLGMCISYAALLTKTNRIYRIFEOGKRSV 691

QY 361 SAPRFISPASQLAITFILISQLLGIQVWVVDPSHVVDFQDQRTLDPRFARGVLKCDI 420
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DB 752 TDLQIICSIGYSILLMVTCTVVAIKTRGVPETFNEAKPIGFTMYTTCIVWLAPIPIFFT 811

QY 481 SOSADKLYIQTTLTVSVLSASVGLMYLMPKVYIILFHPBNVPKRKSLKAVVTAAT 540
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2	75.2	2336	908	2	I49142	metabotropic gluta		
3	71.1	2210	915	2	A49874	metabotropic gluta		
4	68.0	2111.5	551	2	T30806	metabotropic gluta		
5	65.0	2025	874	2	A46742	metabotropic gluta		
6	37.7	1171.5	872	2	JH0561	metabotropic gluta		
7	37.2	1155.5	879	2	JC7160	metabotropic gluta		
8	37.1	1152.5	879	2	JH0562	metabotropic gluta		
9	36.1	1123	1180	2	JC2132	metabotropic gluta		
10	36.1	1122	1199	2	A41939	G protein-coupled		
11	36.0	1118	1212	2	JC2131	metabotropic gluta		
12	36.0	1117.5	1211	2	A42916	metabotropic gluta		
13	35.9	1114.5	1218	2	S711376	glutamate receptor		
14	31.8	989.5	999	2	T27628	hypothetical prote		
15	28.0	871.5	1287	2	T21340	hypothetical prote		
16	22.2	689.5	1078	2	I59362	calcium/polyvalent		
17	21.8	678.5	1079	2	A56715	calcium receptor (
18	21.6	672.5	1085	2	S40476	Ca(2+)-sensing rec		
19	21.5	666.5	1088	2	B56715	calcium receptor (
20	9.9	308.5	858	2	JC7683	taste receptor T1R		
21	9.9	308	1099	2	T16283	hypothetical prote		
22	6.8	212	960	2	JE0356	gamma-aminobutyric		
23	4.3	133	402	2	T29703	hypothetical prote		
24	3.8	118	814	2	JC7389	thyroid stimulating		
25	3.7	115	721	2	AH3417	lpsa protein impo		
26	3.6	112	414	2	B84600	hypothetical prote		
27	3.5	107.5	808	2	T51138	probable glutamate		
28	3.4	107	1034	2	AE3557	acriflavine resista		
29	3.4	106.5	377	2	A69377	Na+/H+ antiporter		

122 IRNVFSGIAGNPTNFENGDPAGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 181
Db
450 IRNVFSGIAGNPTNFENGDPAGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 509
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Db 510 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQYQVDRYTKCTCPYDMRPTE 569
Qy 242 RTSCQPIPIVLEWDSWPAVLPLFLAVVIGIAATLFFVVVTFVRVYNDTPIVVKASGRELSTVL 301
Db 570 RTSCQPIPIVLEWDSWPAVLPLFLAVVIGIAATLFFVVVTFVRVYNDTPIVVKASGRELSTVL 629
Qy 302 LAGIFLCVATTFMLTAEPDLGTCSSRRIFLGLGMSISYAALLTKTNRIYRIFFEQGRKSVS 361
Db 630 LAGIFLCVATTFMLTAEPDLGTCSSRRIFLGLGMSISYAALLTKTNRIYRIFFEQGRKSVS 689
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Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 870 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 912
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C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49142
J. Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory b
A:Reference number: I49142; MUID:952339344; PMID:7722646
A:Accession: I49142
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C:Genetics:
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C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor
Query Match 75.2%; Score 2336; DB 2; Length 908;
Best Local Similarity 74.1%; Pred. No. 9.9e-183; Mismatches 89; Indels 2; Gaps 2;
Matches 432; Conservative 60; Mismatches 89; Indels 2; Gaps 2;
Qy 3 GVSSSLPRMT-SGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRLHAKKGGSHIKKCT 61
Db 327 GAVTILPKRASIDGFDYFRSRTLANNRRNVWFAEFSGNGCKSGSHG-KRNSHIKKCT 385
Qy 62 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHALHAMHRLDCPGRVGLCPRMDPVDGTQLLKY 121
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Qy 122 IRNVFSGIAGNPTNFENGDPAGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 181
Db 446 IRNVFSGIAGNPTNFENGDPAGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 505
Qy 182 GSGQOLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQYQVDRYTKCTCPYDMRPTE 241
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242 RTSCQPIPIVLEWDSWPAVLPLFLAVVIGIAATLFFVVVTFVRVYNDTPIVVKASGRELSTVL 301
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Db 626 LTGIFLCYSITFLMIAAPDTIICSFRIFLGLGMCFSYAALLTKTNRIHRIFFEQGRKSVT 685
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Db 686 APRFISPASQLAITFILISLQLLGICVWFVDPSPSHSVDFQDQRTLDPFRFARGVVKCDIS 745
Qy 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPIFFGTS 481
Db 746 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPIFFGTA 805
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Db 806 QSAEKMYIQTTLTVSMLSASVSLGMLYMPKVYIILFHPQONVQKGRKSFKA VVTAATM 865
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 866 QSKLIQGNDRPNGEVKSSELSTETNTSTKTYYISYSDHSI 908
RESULT 3
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metabotropic glutamate receptor 7 - rat
N:Alternate names: metabotropic glutamate receptor mGluR7
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C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: A49874; I57954
R. Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994
A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coup
A:Reference number: A49874; MUID:94117433; PMID:8288585
A:Accession: A49874
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A:Cross-references: UNIPROT:P35400; GB:D16817; NID:9458728; PIDN:BAA04092.1; PID:9458729
R. Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L. Mol. Pharmacol. 45, 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid
A:Reference number: I57954; MUID:94195260; PMID:8145723
A:Accession: I57954
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
A:Cross-references: EMBL:U06832; NID:9459657; PIDN:AAA20655.1; PID:9459658
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A:Gene: MGLUR7
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor
Query Match 71.1%; Score 2210; DB 2; Length 915;
Best Local Similarity 69.5%; Pred. No. 2e-172; Mismatches 100; Indels 2; Gaps 2;
Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;
Qy 3 GVSSSLPRMT-SGFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRLHAKKGGSHIKKCT 61
Db 332 GATIQPKRAIVGDFDAYFTSRTLENNRRNVWFAEYWEENFNCKLTISGSKEDTDKCT 391
Qy 62 NRERIGQDSAYEQEGKQVQFVIDAVYAMGHALHAMHRLDCPGRVGLCPRMDPVDGTQLLKY 121
Db 392 QGERIGKDSNVEQEGKQVQFVIDAVYAMAHALHMHKDCADYRGVCPCEMEQAGGKLLKY 451
Qy 122 IRNVFSGIAGNPTNFENGDPAGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 180
Db 452 IRNVFSGIAGNPTNFENGDPAGRYDIYQYQLRNGSAEYKIVIGSWTDHLHLRIERQWP 511
Qy 181 PGSSQQLPRISICSLPCQGERKKTIVKGMACCHCEPCTGYQYQVDRYTKCTCPYDMRPTE 240

Db 512 GKGVEIPSSVTLPCPKQQRKTKQGTCCCTCEPCDGYQFQDQEMTCQHCPYDORPNE 571
Qy 241 NRTSCQPIPIVLEWDSWAVLPLFLAVVGIATLFFVYVYVYNDTPIVKASGRELSYV 300
Db 572 NRTGQCNIPILKLEWHSWAVIPVFLAMLGIATIPVMAFIRYNDTPIVRASGRELSYV 631
Qy 301 LLAGIFLCVATTFELMAIEDPLGTCSLRRIIFLGLHMSISYAALLTKTNRIYRIFEOGRSV 360
Db 632 LTTGIFLCYIITFLMAIEDPVAFCFRVFLGLGMCISYAALLTKTNRIYRIFEOGRSV 691
Qy 361 SAPRFPISPAQLAITFILISLQLLGCVMFVVDPSHSVVDFOQRTLDPRFARGVLKCDI 420
Db 692 TAPRLISPTISQAITSLSLISVQLLGVFIWGVDDPNIIIDYDEHKTMNFEQARGVLKCDI 751
Qy 421 SDSLICLLGYMLLMVTCVVAIKTRGVPTFNEAKPIGFTMYTTCIIVWLAFIPIFFT 480
Db 752 TDLQIICSLGYSILLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIIVWLAFIPIFFT 811
Qy 481 SOSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAAT 540
Db 812 AQSADKLYIQTTLTISMLNSASVALGMLYMPKVYIILFHPQONVPRKRSUKAVVTAAT 871
Qy 541 MSNKFTQGNFRPNGEAKSELCELETALATKQTVVYTNHAI 584
Db 872 MSRLSHKPSDRPNGEAKTELCELVDPNSPAKKYVSYNNLVI 915

RESULT 4
T30806
metabotropic glutamate receptor 7 - Fugu rubripes (fragment)
C:Species: Fugu rubripes
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T30806
R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrana, Y.; Wheller, D.; Bishop, G.;
FEBS Lett. 443, 370-374, 1999
A:Title: Three receptor genes for plasminogen related growth factors in the genome of th
A:Reference number: Z20880; MUID:99148833; PMID:10025966
A:Accession: T30806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <COT>
A:Cross-references: UNIPROT:Q9PMQ0; EMBL:AJ010317; NID:e1355235; PID:e1355236; PIDN:CAAC
C:Genetics:
A:Gene: GRM7
A:Note: intron positions not resolved (incomplete sequence)
C:Superfamily: metabotropic glutamate receptor 4

Query Match 68.0%; Score 2111.5; DB 2; Length 551;
Best Local Similarity 68.9%; Pred. No. 1.2e-164;
Matches 376; Conservative 82; Mismatches 87; Indels 1; Gaps 1;

Qy 16 FDRYESSRTLDNRRNIWFAEFWEDNFCKLSRHALKKSHLTKTNRRIGQDSAYBOE 75
Db 1 FDRYESSRTLDNRRNIWFAEFWEDNFCKLSRHALKKSHLTKTNRRIGQDSAYBOE 60

Qy 76 GRVQFVIDAVYANGHALHMHARDLCPGRVGLCPMDPVDGTQLLYIRNVNPSGAGNPV 135
Db 61 GRVQFVIDAVYANGHALHMHARDLCPGRVGLCPMDPVDGTQLLYIRNVNPSGAGNPV 120

Qy 136 TPENGDAPGRYDIYQYQLRN- GSAEYKVGISWTHLHLRIERMOWPGSQQLPRISCSL 194
Db 121 MENGDAPGRYDIYQYQMSNINSGYRNIGQWTHLHLRIERMOWPGSQQLPRISCSF 180

Qy 195 PCQGERKTKVGMACCHCECTGYQYQVDRYCTCTCYDNRPENRTSCQPIVIPLE 254
Db 181 PCQGERKTKVGMACCHCECTGYQYQVDRYCTCTCYDNRPENRTSCQPIVIPLE 240

Qy 255 WDSWAVLPLFLAVVGIATLFFVYVYVYNDTPIVKASGRELSYVLLAGIFLCVATTF 314
Db 241 WSSWAVLPLFLAVVGIATLFFVYVYVYNDTPIVKASGRELSYVLLAGIFLCVATTF 300

Qy 315 MIAEPDLGTCSLRRIIFLGLHMSISYAALLTKTNRIYRIFEOGRSVSAPRFPISPAQLAI 374

Db 301 MIAEPDVACPRRIFLGLHMCISYAALLTKTNRIYRIFEOGRSVTPRFPISPTSQLI 360
Qy 375 TFLISLQLLGCVMFVVDPSHSVVDFOQRTLDPRFARGVLKCDISLISLCLGYSML 434
Db 361 TFLISVQLLGVFIWGVMPHTIIDIYBEQKPNPEFARGVLKCDMSDSLISLCLGYSLV 420
Qy 435 LMVTCVVAIKTRGVPTFNEAKPIGFTMYTTCIIVWLAFIPIFFTSGSADKLYIQTTL 494
Db 421 LMVTCVVAIKTRGVPTFNEAKPIGFTMYTTCIIVWLAFIPIFFTSGSADKLYIQTTL 480
Qy 495 TVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATMSNKFTQGNFRPN 554
Db 481 TVSVLSATVSLGMLYIIPKVYIILFHPQONVPRKRSUKAVVTAATVTRLSQKSDKON 540

Qy 555 GEAKSE 560
Db 541 GESKIE 546

RESULT 5
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46742
R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi,
J. Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor
A:Reference number: A46742; MUID:93280152; PMID:8389366
A:Accession: A46742
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NA>
A:Cross-references: UNIPROT:P35349; GB:D13963; NID:G391856; PIDN:BAA03066.1; PID:G39185
A:Experimental source: retina
A:Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 65.2%; Score 2025; DB 2; Length 871;
Best Local Similarity 68.6%; Pred. No. 2.5e-157;
Matches 371; Conservative 64; Mismatches 102; Indels 4; Gaps 2;

Qy 3 GVSSSLPRMT-SGDRYESSRTLDNRRNIWFAEFWEDNFCKLSRHALKKSHIKKCT 61
Db 319 GAITLPRASIDGDFQYFMTSRLENRRNIWFAEFWENFNCKLTSSGQSDSTRKCT 378

Qy 62 NRERIGQDSAYEQEGKQFVIDAVYANGHALHMHARDLCPGRVGLCPMDPVDGTQLLY 121
Db 379 GEERIGQDSAYEQEGKQFVIDAVYANGHALHMHARDLCPGRVGLCPMDPVDGTQLLY 438

Qy 122 IRNVNPSGAGNPVTPENGDAPGRYDIYQYQLRNGSAE---YKVGISWTHLHLRIERM 178
Db 439 IRNVNPSGAGNPVTPENGDAPGRYDIYQYQLRNGSAE---YKVGISWTHLHLRIERM 198

Qy 179 QWPGSQQLPRISCSLPCQGERKTKVGMACCHCECTGYQYQVDRYCTCTCYDNRP 238
Db 499 RWSGDPHEVPVSQCSLPCQGERKTKVGMACCHCECTGYQYQVDRYCTCTCYDNRP 558

Qy 239 TENRTSCQPIPIVLEWDSWAVLPLFLAVVGIATLFFVYVYVYNDTPIVKASGRELS 298
Db 559 TPNHTGCRPTFVRLTWSSPWAALPLLLAVLGIATLFFVYVYVYNDTPIVKASGRELS 618

Qy 299 YVLLAGIFLCVATTFELMAIEDPLGTCSLRRIIFLGLHMSISYAALLTKTNRIYRIFEOGR 358
Db 619 YVLLAGIFLCVATTFELMAIEDPLGTCSLRRIIFLGLHMSISYAALLTKTNRIYRIFEOGR 678

Qy 359 SVSAPRFPISPAQLAITFILISLQLLGCVMFVVDPSHSVVDFOQRTLDPRFARGVLK 418
Db 679 SVTTPPFPISPTSQLIITFLISVQLLGVFIWGVMPHTIIDIYBEQKPNPEFARGVLK 738

Qy 419 DISLSLCLGYSMLLMVTCVVAIKTRGVPTFNEAKPIGFTMYTTCIIVWLAFIPIFF 478

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Db DMSDLISGLGYSLLMVTCTVVAIKARGVPETFNFAKPIGFTMYTTCIWLAFVPIFF 798
Qy GTSQADKLYIQTTLTVSVLSASVSLGMLYMPKYVLIILPHPNQVPRKRSLSKAVVTA 538
Db GTSQAEKIYIQTTLTVSVLSASVSLGMLYMPKYVLIILPHPNQVPRKRSLSKKTSTM 858
Qy 539 A 539
Db 859 A 859

RESULT 6
JH0561
metabotropic glutamate receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0561
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002; PMID:1309649
A:Accession: JH0561
A:Molecule type: mRNA
A:Residues: 1-872 <TAN>
A:Cross-references: UNIPROT:p31421
A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
F:568-590/Domain: transmembrane #status predicted <TRI>
F:608-625/Domain: transmembrane #status predicted <III>
F:637-655/Domain: transmembrane #status predicted <III>
F:680-700/Domain: transmembrane #status predicted <TRV>
F:726-747/Domain: transmembrane #status predicted <TRV>
F:761-782/Domain: transmembrane #status predicted <TVI>
F:795-819/Domain: transmembrane #status predicted <VII>
F:203,286,338,402,547/Binding site: carbohydrate (Aan) (covalent) #status predicted
F:601,675,827,843/Binding site: phosphate (Ser) (covalent) #status predicted
F:832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 37.7%; Score 1171.5; DB 2; Length 872;
Best Local Similarity 44.3%; Pred. No. 1.5e-87;
Matches 249; Conservative 75; Mismatches 197; Indels 41; Gaps 10;

Qy 4 VSSSLPTMTSGDFRYFSSTLNNRRNIWFAEFWEDNFHCKL-----SRHALKKGSHIK 58
Db ITIELASYPISDFASYFQSLDPWNNRNPNWFRFEWFRHCSFRQDCAAHSRA----- 369

Qy 59 KCTNRRTGQDSAYEQEGKQFVDVAVYMGHALHAMHRLDLCPRVGLCPRMDDPVDGTQL 118
Db -----VPEQESKIMFVNNAVYAMAHALHMKQRTLCPNTHLLCDAMRVNGRLL 418

Qy 119 LK-YIRNVNFS-----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 419 YKDFVLNVKFPAPPAFTDDEVRDFRGGIGRINIFTY-LRAGSGRYRYQKGYWAEQ 477
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 171 LHLRIERMQW--PGSGQOLPRISCSLPQCPGERKKTKVGMACCWHCEBCTGYQYQVDRYT 228
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 478 LTLDTSFIPWASPSAG-PLPASRCEPCLQNEVKSVPQGEVCCWLCIPCPYEVRLDEFT 536
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 229 KCTPYDMRPTENRTSCQPIPIVKLEWDSPNVAVLPLAVVGVIAATLPLVAVVTFVRYNDTP 288
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 537 CADCGLGWPNASLTGCFELPQEVIRMGDVAWAGVPTIACIGALATLFLVGVFVRHNATP 596
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 289 IVKASGRELTVYLAGIFLCVATFLMTAEPLDGLTCSLRIRIFLGLGMSISVAALLTKNRIYFEQGR 348
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 597 VKASGRELTVYLAGIFLCVATFLMTAEPLDGLTCSLRIRIFLGLGMSISVAALLTKNRIYFEQGR 656
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170

Qy 349 IYRIFEQGRSVSPAPRFTSPASQLAITFILISQLLIGICVWFVVDPSHVVDFDQRTLD 408
Db -----GIAGNPVTFNENGDPGRYDIYQYQLRNGSABYKYV--IGSWTDH 170
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Db 657 IARIFGGAREGAQRPFISPASQVAICLALISQQLLIIVAAWLVVEAPGT-----GKETAP 711
Qy PRPARGLVKCDISDLSLILCLLYGSMILMVTCTVVAIKRGVPETFNFAKPIGFTMYTTCI 468
Db ERREVTLRNCNRDASWIGSLAYNVLLIALCTLYAFTRKCPENFNAKPIGFTMYTTCI 771
Qy VWLAPIPFFGTQSADKLYIQTTLTVSVLSASVSLGMLYMPKYVLIILPHPNQVPRKRS 528
Db IWLAFLPFIVYVTSDD---YRVQITTMCMVSVLSGSLVGLCLFAPKLHILFQPKQNVVSH 828

Qy 529 KRSLSKAVVTAATWNSKFTQKGN 550
Db 829 RAPTSTREFGSAAPRASANLGQGS 850

RESULT 7
JC7160
metabotropic glutamate receptor subtype 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C:Accession: JC7160
R:Minooshima, T.; Nakanishi, S.
J. Biochem. 126, 889-896, 1999
A:Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3
A:Reference number: JC7160; MUID:20012997; PMID:10544282
A:Accession: JC7160
A:Molecule type: DNA
A:Residues: 1-879 <MIN>
A:Cross-references: GB:AF170696
C:Genetics:
A:Gene: mGluR3
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>
F:577-599/Domain: transmembrane #status predicted <TM1>
F:614-634/Domain: transmembrane #status predicted <TM2>
F:646-664/Domain: transmembrane #status predicted <TM3>
F:689-709/Domain: transmembrane #status predicted <TM4>
F:735-756/Domain: transmembrane #status predicted <TM5>
F:770-791/Domain: transmembrane #status predicted <TM6>
F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 37.2%; Score 1155.5; DB 2; Length 879;
Best Local Similarity 42.8%; Pred. No. 3.1e-86;
Matches 236; Conservative 85; Mismatches 195; Indels 35; Gaps 9;

Qy 6 SSLLPTMTSGDFRYFSSTLNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCTNRER 65
Db ASHPVRQ---FDRYFQSLNPNYNNHRNPWFRDFWEQKFCQSLQ----NKRNRHQICDKHLA 378

Qy 66 IGODSAYEQEGKQFVDVAVYMGHALHAMHRLDLCPRVGLCPRMDDPVDGTQLLK-YIRN 124
Db I-DSSNYEQESKIMFVNNAVYAMAHALHMKQRTLCPNTHLLCDAMKLDGKKLYKDYLLK 437

Qy 125 VNFSGI-----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 438 INFAPNPNKGADSIYKFDYTGDMGRYVNFVNFQHIGGKYSYLKVGHWAEATLYLDVDSI 497
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 179 QWPGSGQOLPRISCSLPQCPGERKKTKVGMACCWHCEBCTGYQYQVDRYTCKTCYDMRP 238
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 498 HW--SRNSVPTSQSDPCAPNEMKNMQPDGVCCWICIPCIBPYEYLVDFEFTCMDCGPGQWP 555
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 239 TENRTSCQPIPIVKLEWDSPNVAVLPLAVVGVIAATLPLVAVVTFVRYNDTPVVKASGREL 298
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 556 TADLSGCYNLPEDYIRWEDAWAIGPVTIACIGFMCCTCIVITVFIKHNTPLVVKASGREL 615
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 299 YVLLAGIFLCVATFLMTAEPLDGLTCSLRIRIFLGLGMSISVAALLTKNRIYRIFEQGR 358
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 616 YILLFGVSLSCVMTFFIAKPSPVICALRGLGLTGSFAICYSALLTKTNCIARIFDGVKN 675
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178

Qy 359 SVSAPRFTSPASQLAITFILISQLLIGICVWFVVDPSHVVDFDQRTLDPRFARGVLKC 418
Db -----AGNPVTFNENGDPGRYDIYQYQLRNGSABYKYVIGSWTDHHLRIERM 178
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Db 676 GAORPKFISPSQVFCIGLILVQVVMVSWLILETPGT-----RRYTLPEKRETVILKC 730
 QY 419 DISDLSLICLLGYSMMLMTCTVYAIKTRGVPTNEAKPIGFTMYTTCIVWLAFIPIFF 478
 Db 731 NVKSSMLISLTVDVVLVILCTVYAFKTRKCPENFEAKFIPTGFTMYTTCIVWLAFIPIFF 790
 QY 479 QTSQADKLYIQTTTLTVSVLSASVSLGMLYMPKYIILFHPQNVPRKRSLSKAVTTA 538
 Db 791 VTSSD---YRVQTTMCISVLSGFWVLGCLFAPKVIHLVFPQKN-----VVTH 837
 QY 539 ATMSNKFTQKG 549
 Db 838 RLHLNRFVSUG 848

RESULT 8
 JH0562
 metabotropic glutamate receptor 3 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JH0562
 R.Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 Neuron 8, 169-179, 1992
 A:Title: A family of metabotropic glutamate receptors.
 A:Reference number: JH0561; MUID:92110002; PMID:1309849
 A:Accession: JH0562
 A:Molecule type: mRNA
 A:Residues: 1-879 <UNP>
 A:Cross-references: UNIPROT:P31422
 A:Experimental source: brain
 C:Comment: This protein is coupled to a G protein and evokes a variety of functions by
 C:Superfamily: metabotropic glutamate receptor 4
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
 F:577-599/Domain: transmembrane #status predicted <TRI>
 F:614-634/Domain: transmembrane #status predicted <TII>
 F:646-664/Domain: transmembrane #status predicted <III>
 F:689-709/Domain: transmembrane #status predicted <TIV>
 F:735-756/Domain: transmembrane #status predicted <TVI>
 F:770-791/Domain: transmembrane #status predicted <TVI>
 F:804-828/Domain: transmembrane #status predicted <VII>
 F:209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 37.1%; Score 1152.5; DB 2; Length 879;
 Best Local Similarity 42.8%; Pred. No. 5.4e-86;
 Matches 236; Conservative 84; Mismatches 196; Indels 35; Gaps 9;

QY 6 SSSLPTMTSGDFRYSRTLDNNRRNINFAEFWEDNFHCKLSRHALKKGSHIKKCTNR 65
 Db 326 ASHPVRQ---FDRYFQSLNPNYNNRNPFRDFWEQKFCQSLQ-----NKRNRQVCDKHLA 378
 QY 66 ICQDSAYEKGKQVVIDAVYANGHALHAMHRDLCPGRVGLCPMDPVDGTQLLK-YR 124
 Db 379 I-DSSNYEQESKIMFYVNAVYAMAHAKMQRTLCPTNTTKLCDAMKILDGKLYEYLLK 437
 QY 125 VNFSGI-----AGNPVTENEGDAPGRYDIYQYQLRNGSAEYKVGISWTDLHLRIERM 178
 Db 438 INFTAPFNKAGDSLVKEDTGDGGRYNNVNLQQTGGKYSYLVKGHWAEFLSLDSDSI 497
 QY 179 QWPGSQQLPRGISLPCQPGERKKTVMGMAWCHCEPCTGYQYQVDRYTCCTCPYDMRP 238
 Db 498 HW--SRNSVPTSQCDPCAPNEMKNQPGDVCCWICIPCEPYEVLVDEFTCDCCGQWP 555
 QY 239 TNRNRSQPIPIVKLEWDSFVAVLPFLAVVGIATFLFVVVTFVRYNDTPIVKASGRELS 298
 Db 556 TADLSGYNLPEDYIKWEDAWAIGPVTIACLGFLCTCIVITFVKHNTPLVKASGRELC 615
 QY 299 YVLLAGIFLCYATTFLMIAEPDLGTCSLRIFLGLGMSISYAALLTKTNRIYRIEQQGR 358
 Db 616 YILLFGVSLSYCWTFPFIAKPSVICALRRLLGLTSFAICYALLTKTNRIARIPGVKN 675

QY 359 SVSAPRFPISPAQLAITFILLISQLLIGTCVWFVDPDSHVSVDFOQDORTLDPFARGVLKC 418
 Db 676 GAORPKFISPSQVFCIGLILVQVVMVSWLILETPGT-----RRYTLPEKRETVILKC 730
 QY 419 DISDLSLICLLGYSMMLMTCTVYAIKTRGVPTNEAKPIGFTMYTTCIVWLAFIPIFF 478
 Db 731 NVKSSMLISLTVDVVLVILCTVYAFKTRKCPENFEAKFIPTGFTMYTTCIVWLAFIPIFF 790
 QY 479 QTSQADKLYIQTTTLTVSVLSASVSLGMLYMPKYIILFHPQNVPRKRSLSKAVTTA 538
 Db 791 VTSSD---YRVQTTMCISVLSGFWVLGCLFAPKVIHLVFPQKN-----VVTH 837
 QY 539 ATMSNKFTQKG 549
 Db 838 RLHLNRFVSUG 848

RESULT 9
 JH2132
 metabotropic glutamate receptor 5 A - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
 C:Accession: JH2132
 R.Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
 Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
 A:Title: Molecular cloning and the functional expression of two isoforms of human metab
 A:Reference number: JH2131; MUID:94197696; PMID:7908515
 A:Accession: JH2132
 A:Molecule type: mRNA
 A:Residues: 1-1180 <MIN>
 C:Comment: This protein is coupled to guanine nucleotide binding proteins.
 C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
 F:580-604/Domain: transmembrane #status predicted <TM1>
 F:617-637/Domain: transmembrane #status predicted <TM2>
 F:644-664/Domain: transmembrane #status predicted <TM3>
 F:694-714/Domain: transmembrane #status predicted <TM4>
 F:738-759/Domain: transmembrane #status predicted <TM5>
 F:773-794/Domain: transmembrane #status predicted <TM6>
 F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 36.1%; Score 1123; DB 2; Length 1180;
 Best Local Similarity 39.8%; Pred. No. 2e-83;
 Matches 229; Conservative 111; Mismatches 198; Indels 38; Gaps 9;

QY 3 GVSSSLPTMTSGDFRYSRTLDNNRRNINFAEFWEDNFHCKLSRHALKKGSHIKKCTN 62
 Db 324 GITIKLQSPDVKWFDDYILKLRPETNHRNPWFQEFQHRFQCLRGFPQENSKYNTKNS 383
 QY 63 RERIGQDSAYEKGKQVVIDAVYANGHALHAMHRDLCPGRVGLCPMDPVDGTQLLK 122
 Db 384 --SLTLKTHVQDSKMGFVINAISYMAVGLHNMQMSLCPGYAGLGDAMKPIDGRKLLES 441
 QY 123 RNVSFSGIAGNPVTENEGDAPGRYDIYQY-QLRNGSAEYKVGISWTDLHLRIERM 181
 Db 442 MKNFTGVSQDITLFDENGDSGRYEIMNFKEGMDYFDYINVSWS-DNGELKMDDEW 500
 QY 182 GSGQQLPRGISLPCQPGERKKTVMGMAWCHCEPCTGYQYQVDRYTCCTCPYDMRP 240
 Db 501 SKKSNIIIRSCVCEPKGQIKVIRKEVSCCTCTPCKENEYVDEYTCACKQLGSWPTD 560
 QY 241 NRTSCQPIPIVKLEWDSFVAVLPFLAVVGIATFLFVVVTFVRYNDTPIVKASGRELS 300
 Db 561 DLTGCDLIPVQYLRWGDPEPIAAVAVFACGLLALTFTVTFVTFIYRDTTPVKSSREL 620
 QY 301 LLAGIFLCYATTFLMIAEPDLGTCSLRIFLGLGMSISYAALLTKTNRIYRIEQQGR 360
 Db 621 ILAGICLGLYCTFCLIAKPKQYCYQLRIGIGLSFAMYSALVTKTNRILARILAGSKKI 680
 QY 361 --SAPRFPISPAQLAITFILLISQLLIGTCVWFVDPDSHVSVDFOQDORTLDPFARGVLKC 418
 Db 681 CTXKPRFWSACQLVIAFILLICQIIGIIVAFIMEPDDIMHDY-----PSIREVYLIC 733
 QY 419 DISDLSLICLLGYSMMLMTCTVYAIKTRGVPTNEAKPIGFTMYTTCIVWLAFIPIFF 478

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Db 734 NNTNLGVVTPGLGYNGLLILSCTFYAFKTRNVPANFNEAKYIAFTMYTTCIIWLAFAPIYF 793
Qy 479 GTSQSADKLYIQTTTLTVSVLSASVSIGMLYMPKVYIILFHPHQNVPRKRSI----- 528
Db 794 GSN-----YKIITTCFAVSLSATVALGCMFVKPYIILAKPERNVSFAFTTSTVVRMH 846
Qy 529 ---KRLKAVVTAATMSNKFQKGN----PRPNGEA 557
Db 847 VODGKSSSAARSSSLVNLWKRGSGETLRSNGKS 882

RESULT 10
A41939
G protein-coupled glutamate receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A41939; S15362
R:Houamed, K.M.; Kujiper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill,
Science 252, 1318-1321, 1991
A>Title: Cloning, expression, and gene structure of a G protein-coupled glutamate receptor
A:Reference number: A41939; MUID:9202526; PMID:1656524
A:Accession: A41939
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-1199 <HOU>
A:Cross-references: UNIPROT:P23385; GB:M61099; NID:g397806; PIDN:AAAL9497.1; PID:g204460
A:Experimental source: cerebellum
A>Note: sequence extracted from NCBI backbone (NCBIP:60785)
R:Masu, M.; Tanabe, Y.; Tachida, K.; Shigemoto, R.; Nakanishi, S.
Nature 349, 760-765, 1991
A>Title: Sequence and expression of a metabotropic glutamate receptor.
A:Reference number: S15362; MUID:91156047; PMID:1847995
A:Accession: S15362
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1199 <MAS>
A:Cross-references: EMBL:X57569; NID:g56646; PIDN:CAA40799.1; PID:g56647
A:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 36.1%; Score 1122; DB 2; Length 1199;
Best Local Similarity 38.9%; Pred. No. 2.4e-83;
Matches 239; Conservative 106; Mismatches 208; Indels 62; Gaps 12;

Qy 3 GVSSSLPTMTSGPDYFSSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCTN 62
Db 337 GITIKLQSPVQKPFDDYILKLPETNRNPFQFQHRFOCRLEGPEQNSKNKTCNS 396
Qy 63 RERIGQDSAYEQEGKQVQFIDAVYAMGHALHAMHRDLCPRVGLCPRPMDPVDGTQLLKYI 122
Db 337 NESLEEN--YVQDSKMGFVINAIYMAHGLQNMHHALCPGHVGLCDAMKPIDGRKLLDPL 454
Qy 123 RNVNFSGIAGNPVTFNENGDAFGYDIYQYQLRNGSA-EYKVGISWTDH-LHLRIERMQW 180
Db 455 IKSSFPVGSVEEWFDEKGDAPGRYDINLQYTEANRYDYVHVGVTHGVLNIDDKYIOM 514
Qy 181 PEGSQQLPRSTCLSPQCGGERKKTVKG-MACQWCHCEPCTGYQYQVDRYTKCTCPYDMRPT 239
Db 515 NKSG--MVRVSCSEPLGQIKVIRKGEVSCCWICTACKENEFVQDEFTCRACDLGMPN 572
Qy 240 ENRTSCQPIPIVKLEWDSFPAVLPLFLAVVGAATLFFVVVTFVRYNDTPIVKASGRELSY 299
Db 573 AELTGCEPIPVRYLEWSDIESIIAIFASCLGILVTLFVLIVYRDTPVVKSSRELCTY 632
Qy 300 VLLAGIFLCYATTFMLIAEPDLGTCSLRRIFILGLGMSISYAALLTKTNRIYRIFEQGKRS 359
Db 633 IILAGIFLGYVCPFTLIAKPTTSCYLQRLVGLSSAMCYSALVTKTNRIARILAGSKK 692
Qy 360 VSA---PRFISPASQLAIFILISLQILGICVWFVVDPSHVSVDQDRTLDPRFARGVLK 417
Db 693 ICTRKPRFMSAWAQVIAISILISVQLTLVTLVLIIMEPPMILSY-----PSIKEVYLI 745
Qy 418 CDISLSLICLLGYSMMLMWTCVVAIKTRGVPETFNEAKPIGFTMYTTCIIWLAFAPIF 477
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Db 746 CNTSNLGWAPVGVNGLLINSCTFYAFKTRNVPANFNEAKYIAFTMYTTCIIWLAFAPIY 805
Qy 478 FGTQSADKLYIQTTTLTVSVLSASVSIGMLYMPKVYIILFHPHQNVPRKRSI----- 532
Db 806 FGSN-----YKIITTCFAVSLSATVALGCMFVKPYIILAKPERNV-----RSAFTTSD 854
Qy 533 -----KAVVTAATMSNKFQKGN----GNFRNGEAKS-----ELC 562
Db 855 VVRMHVGDGKLPCHSNTFLNIFRKKPGAGNANSNGKSVSWSEPGGROAPKGQHVWQRLS 914
Qy 563 ENLETPALATKQTYV 577
Db 915 VHVKTNETACNQTA 929

RESULT 11
JC2131
metabotropic glutamate receptor 5 B - human
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2131
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A>Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131; MUID:94197696; PMID:7908515
A:Accession: JC2131
A:Molecule type: mRNA
A:Residues: 1-1212 <MIN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
E:580-604/Domain: transmembrane #status predicted <TM1>
E:617-637/Domain: transmembrane #status predicted <TM2>
E:644-664/Domain: transmembrane #status predicted <TM3>
E:694-714/Domain: transmembrane #status predicted <TM4>
E:738-759/Domain: transmembrane #status predicted <TM5>
E:773-794/Domain: transmembrane #status predicted <TM6>
E:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 36.0%; Score 1118; DB 2; Length 1212;
Best Local Similarity 39.4%; Pred. No. 5.2e-83;
Matches 231; Conservative 111; Mismatches 197; Indels 48; Gaps 10;

Qy 3 GVSSSLPTMTSGPDYFSSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCTN 62
Db 324 GITIKLQSPVQKPFDDYILKLPETNRNPFQFQHRFOCRLEGPEQNSKNKTCNS 383
Qy 63 RERIGQDSAYEQEGKQVQFIDAVYAMGHALHAMHRDLCPRVGLCPRPMDPVDGTQLLKYI 122
Db 384 --SILTAKTHVQDSKMGFVINAIYMAVGLHNMQMSLCPGVAGLCDAMKPIDGRKLLSL 441
Qy 123 RNVNFSGIAGNPVTFNENGDAFGYDIYQY-QLRNGSAEYKVGISWTDHHLRIERMQWP 181
Db 442 MKTNFTGVSQDITLFDENGSDSPGRYEIMNFKMGKQYFDYINVGSW-DNGELMKDDDEVW 500
Qy 182 GSGQQLPRSTCLSPQCGGERKKTVKG-MACQWCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
Db 501 SKSNIIIRVSCSEPEKQIKVIRKGEVSCCWTCTPKENEYVDEYTCACQLGSWPTD 560
Qy 241 NRTSCQPIPIVKLEWDSFPAVLPLFLAVVGAATLFFVVVTFVRYNDTPIVKASGRELSY 300
Db 561 DLTGCDLIPVQLRWGDPPEIAAVFACLGALLATLFTVTVFIIYRDTFVVKSSRELCTY 620
Qy 301 VLLAGIFLCYATTFMLIAEPDLGTCSLRRIFILGLGMSISYAALLTKTNRIYRIFEQGKRS 360
Db 621 ILAGICGLYCTFCLIAKPKQIYCYLQRIIGLSPAMSYSALVTKTNRIARILAGSKKI 680
Qy 361 --SAPRFPISASQLAIFILISLQILGICVWFVVDPSHVSVDQDRTLDPRFARGVLK 418
Db 681 CTKKPRFMSACQVIAFILIICIQIIGIIVAFINEPPDIMDY-----PSIREVYLI 733
Qy 419 DISLSLICLLGYSMMLMWTCVVAIKTRGVPETFNEAKPIGFTMYTTCIIWLAFAPIF 478
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Db 734 NITNLGVVTPGLYNGLLILSCTFYAPKTRNVNPNFNEAKYIAFTMYTTCIIWLAFVPIYF 793
Qy 479 GTSQSADKLYIQTTLTVSVLSASVSLGMLYMPKYYIILFHPQNVPKR----- 528
Db 794 GSN-----YKIITMCFVSLSATVALGCMFVPKVIYIILAKPERNVRSFAFTTSTVVRMH 846
Qy 529 ---KRSLKAVVTAATNSNFTQGNFRPNCEA-----KSEL 561
Db 847 VDGKSSSAASRSSSLVNLWKRGS---SGETLRYKDRLLAOKHSBI 890

RESULT 12
A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42916
R:Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 cDNA
A:Reference number: A42916; MUID:92317054; PMID:1320017
A:Accession: A42916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <AB>
A:Cross-references: UNIPROT:P31424; GB:D10891; NID:G220813; PIDN:BAA01711.1; PID:di100218
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBI:107750)
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 36.0%; Score 1117.5; DB 2; Length 1171;
Best Local Similarity 40.1%; Pred. No. 5:5e-83;
Matches 230; Conservative 109; Mismatches 198; Indels 37; Gaps 9;

Qy 3 GVSSSLPTMTSGDFRYFSRSLDNNRNINWPAEFWEDNFHCKLSRHALKKGSHIKCTN 62
Db 323 GITIKLQSDPVKDFDYILKLPETNLNPNWQFQFHWQHRFQCKLEGAENSKYNTCS 382

Qy 63 RERIGQDSAYEQBGKQVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPMPDPVDTQLLKYI 122
Db 383 --SLTERTHVQDSKMGFVINAIYSWAYGLHMQMSLCPGYAGLCDAMKPIDGRKLLDSL 440

Qy 123 RVNFGSIAGNPVTNENGADPRDIYQY-QLRNGSABYKVGISWTDLHLRIERMQWP 181
Db 441 MKTNFTGVSGLMFLDENGSPGRYBIMNFKMGKDPYDYNVGSW-DNGELKMDDDYV 499

Qy 182 GSGQQLPRISICSLPCQGERKKTVKG-MACCVHCEPCTGYQYQVDRYTCTCPYDMRPT 240
Db 500 SKNNIIRSVCEPCEKQIKVIRKEVSCCTCTPCKENEYVDFEYTCACQLGSWPTD 559

Qy 241 NRTSCQPIPIVKLEWDSWAVLPLFLAVVGIATLFFVYVTFVRYNDTPIVKASGRELSYV 300
Db 560 DLTGCDLIPVQVLRWGDPEPIAAVVPACGLLATLFTVTFIYIRDTVPVKSSRELCTY 619

Qy 301 LLAGIFLCYATTFMLAEPDLGTCSLRRIFPLGLGMSISYAALLTKNRIYRIFEQGRSV 360
Db 620 ILAGICGLGYLCTFCLAKPKQICYLQRIIGLSPAMSYALSALVTKTNRIARLAGSKKI 679

Qy 361 --SAPFISPAQLATTEILISLQGLGICVWFVVDPSHVSVDQDQRTDPRFARGVLAK 418
Db 680 CTYKPRFMSACQLVJAFILICIQUGIIVALPEPDIIMHDY-----PSIREVFLIC 732

Qy 419 DISLSLCLLGYSMMLMTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAFIPIFP 478
Db 733 NITNLGVVTPGLYNGLLILSCTFYAPKTRNVNPNFNEAKYIAFTMYTTCIIWLAFVPIYF 792

Qy 479 GTSQSADKLYIQTTLTVSVLSASVSLGMLYMPKYYIILFHPQNVPKR----- 528
Db 793 GSN-----YKIITMCFVSLSATVALGCMFVPKVIYIILAKPERNVRSFAFTTSTVVRMH 845

Qy 529 ---KRSLKAVVTAATNSNFTQGNFRPNCEA 559
Db 846 VDGKSSSAASRSSSLVNLWKRGS---SGETLS 876

RESULT 13

S71376

glutamate receptor homolog - cherry salmon

C:Species: Oncorhynchus masou (cherry salmon)

C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004

C:Accession: S71376

R:Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.

FEBS Lett. 392, 71-76, 1996

A:Title: Cloning and characterization of a bifunctional metabotropic receptor activated

A:Reference number: S71376; MUID:96354880; PMID:8769318

A:Accession: S71376

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1218 <KUB>

A:Cross-references: UNIPROT:Q90ZP3

C:Keywords: glycoprotein; phosphoprotein

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F:640-660/Domain: transmembrane #status predicted <TM2>

F:672-690/Domain: transmembrane #status predicted <TM3>

F:717-737/Domain: transmembrane #status predicted <TM4>

F:761-782/Domain: transmembrane #status predicted <TM5>

F:796-817/Domain: transmembrane #status predicted <TM6>

F:826-850/Domain: transmembrane #status predicted <TM7>

F:104,233,403,525,757/Binding site: carbonylrate (Asn) (covalent) #status predicted

F:636,699,961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pr

F:705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

F:892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predi

Query Match 35.9%; Score 1114.5; DB 2; Length 1218;

Best Local Similarity 41.7%; Pred. No. 1e-82;

Matches 220; Conservative 97; Mismatches 189; Indels 21; Gaps 7;

Qy 3 GVSSSLPTMTSGDFRYFSRSLDNNRNINWPAEFWEDNFHCKLSRHALKKGSHIKCTN 62

Db 347 GITVKLHSEEVTSFDYFLKRLNTNPNWPFQFHWQHRFQCKRIPOHPLNNYRNKCSG 406

Qy 63 RERIGQDSAYEQBGKQVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPMPDPVDTQLLKYI 122

Db 407 YESL--EDNYVQDSKMGFVINAIYAMAQGLHDMHSLCPGHVGLCKAMPIDGSQLLEFL 464

Qy 123 RVNFGSIAGNPVTNENGADPRDIYQY-QLRNGSABYKVGISWTDLHLRIERMQWP 181

Db 465 MRTSFTGVSGLMFLDENGSPGRYBIMNLQYVEPQAFDYNVGSWHGEG-QLSIDDYMMQ 523

Qy 182 GSGQQLPRISICSLPCQGERKKTVKG-MACCVHCEPCTGYQYQVDRYTCTCPYDMRPT 240

Db 524 INRSDNVLSVCEPCEKQIKVIRKEVSCCTCTACKONEIVQDEFTCTACDLGWDPD 583

Qy 241 NRTSCQPIPIVKLEWDSWAVLPLFLAVVGIATLFFVYVTFVRYNDTPIVKASGRELSYV 300

Db 584 ELEGECEPITLRYLEWGNPESIVQVVPACGLILVTSFVTFIVLYRDTVPVKSSRELCTY 643

Qy 301 LLAGIFLCYATTFMLAEPDLGTCSLRRIFPLGLGMSISYAALLTKNRIYRIFEQGRSV 360

Db 644 ILAGIFLGYLCPFTLIAQFTVASCYLQRLVGLSATMCSYALSALVTKTNRIARLAGSKKI 703

Qy 361 SA--PRFISPAQLATTEILISLQGLGICVWFVVDPSHVSVDQDQRTDPRFARGVLAK 418

Db 704 CTRKPRFMSACQLVJAFILICIQUGIIVALPEPDIIMHDY-----PSIREVFLIC 756

Qy 419 DISLSLCLLGYSMMLMTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAFIPIFP 478

Db 757 NTSTVGWVAPLGYNGLLIMSCYYAFKTRNVPANFNEAKYIAFTMYTTCIIWLAFVPIYF 816

Qy 479+ GTSQSADKLYIQTTLTVSVLSASVSLGMLYMPKYYIILFHPQNV 525

Db 817 GSN-----YKIITTSFVSLSVTVALGCMFSPKVIYIILAKPERNV 856

RESULT 14

T27628

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2005, 18:07:59 ; Search time 47 Seconds
(without alignments)
927.554 Million cell updates/sec

Title: US-10-828-332-7
Perfect score: 3107
Sequence: 1 MFGVSSSLPTRMTSGDRYF.....LETPALATKQTVVYVTHAI 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	98.2	604	US-09-820-809-13	Sequence 13, Appli
2	3050.5	98.2	912	PCT-US91-09422-19	Sequence 19, Appli
3	3004.5	96.7	912	US-08-617-785-2	Sequence 2, Appli
4	3004.5	96.7	912	US-09-641-318-2	Sequence 2, Appli
5	3004.5	96.7	912	US-09-817-464-2	Sequence 2, Appli
6	2370	76.3	908	US-08-855-146-2	Sequence 2, Appli
7	2328	74.9	908	US-08-823-110-1	Sequence 1, Appli
8	2328	74.9	908	US-08-604-298-1	Sequence 1, Appli
9	2219	71.4	915	US-08-617-785-12	Sequence 12, Appli
10	2219	71.4	915	US-09-817-464-12	Sequence 12, Appli
11	2210	71.1	915	US-08-453-862-2	Sequence 2, Appli
12	2210	71.1	915	US-08-452-734A-2	Sequence 2, Appli
13	2210	71.1	915	US-08-176-401B-2	Sequence 2, Appli
14	2210	71.1	915	PCT-US94-14989-2	Sequence 2, Appli
15	2191.5	70.5	867	US-08-617-785-4	Sequence 4, Appli
16	2191.5	70.5	867	US-08-617-785-2	Sequence 4, Appli
17	2191.5	70.5	922	US-09-817-785-14	Sequence 14, Appli
18	2191.5	70.5	922	US-09-817-464-14	Sequence 14, Appli
19	2052.5	66.1	877	US-08-407-875-2	Sequence 2, Appli
20	2052.5	66.1	877	US-09-277-858-2	Sequence 2, Appli
21	2040.5	65.7	877	US-09-126-280-2	Sequence 2, Appli
22	1861.5	59.9	481	US-08-617-785-8	Sequence 8, Appli
23	1861.5	59.9	481	US-08-617-464-8	Sequence 8, Appli
24	1172.5	37.7	872	US-08-337-797A-2	Sequence 2, Appli
25	1172.5	37.7	872	US-09-258-523-2	Sequence 2, Appli
26	1155.5	37.2	879	US-08-794-158-2	Sequence 2, Appli
27	1148.5	37.0	879	US-08-072-574-6	Sequence 6, Appli

28	1148.5	37.0	879	1	US-08-486-270-6	Sequence 6, Appli
29	1148.5	37.0	879	3	US-08-367-284-6	Sequence 6, Appli
30	1148.5	37.0	879	4	US-09-153-757-6	Sequence 6, Appli
31	1148.5	37.0	879	4	US-09-459-715-6	Sequence 6, Appli
32	1129	36.3	1194	3	US-08-538-526-1	Sequence 1, Appli
33	1123.5	36.2	1056	2	US-08-687-289A-8	Sequence 8, Appli
34	1123.5	36.2	1056	4	US-09-435-897-8	Sequence 8, Appli
35	1122	36.1	1199	1	US-08-041-538-2	Sequence 2, Appli
36	1122	36.1	1199	1	US-08-463-642-2	Sequence 2, Appli
37	1122	36.1	1199	1	US-08-455-602-2	Sequence 2, Appli
38	1122	36.1	1199	2	US-08-465-157-2	Sequence 2, Appli
39	1122	36.1	1199	5	PCT-US91-09422-2	Sequence 2, Appli
40	1121.5	36.1	878	4	US-09-826-509-347	Sequence 347, App
41	1121.5	36.1	906	1	US-08-486-270-2	Sequence 2, Appli
42	1121.5	36.1	906	3	US-08-367-264-2	Sequence 2, Appli
43	1121.5	36.1	906	4	US-09-153-757-2	Sequence 2, Appli
44	1121.5	36.1	906	4	US-09-459-715-2	Sequence 2, Appli
45	1121.5	36.1	1043	4	US-09-695-481-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-820-809-13
; Sequence 13, Application US/09820809
; Patent No. 6608176
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARI, NIRUPA
; APPLICANT: ROBER, STEPHEN D.
; TITLE OF INVENTION: TASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
; FILE REFERENCE: 70373/275576
; CURRENT APPLICATION NUMBER: US/09/820,809
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,454
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-820-809-13

Query Match	98.2%	Score 3050.5;	DB 4;	Length 604;
Best Local Similarity	98.6%	Pred. No. 2.7e-300;		
Matches	575;	Conservative	2;	Mismatches 5; Indels 1; Gaps 1;
QY	3	GVSSSLPRMT-SGDRYFSSRTLDNNRNTWFAFWEDNFHCKLSRHALKKGSHIKKCT	61	
Db	22	GAVTILPKRMSVRGDRYFSSRTLDNNRNTWFAFWEDNFHCKLSRHALKKGSHIKKCT	81	
QY	62	NRERIGDSAYEKGKQVFVDVAVYMGHALHMHARDLCPGRVGLCPRMDPVDGTQLLKY	121	
Db	82	NRERIGDSAYEKGKQVFVDVAVYMGHALHMHARDLCPGRVGLCPRMDPVDGTQLLKY	141	
QY	122	IRNVNFSIAGNPVTFFNENGDPGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMQWP	181	
Db	142	IRNVNFSIAGNPVTFFNENGDPGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMQWP	201	
QY	182	SGGQOLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQYQVDRYTKTCYDMRPTEN	241	
Db	202	SGGQOLPRISICSLPCQGERKKTVMKMACCHCEPCTGYQYQVDRYTKTCYDMRPTEN	261	
QY	242	RTSCOPIPIVKLEWDSFWAVLPLAVVGIATLFWVTVFYNDTPVVKASGRELSSYL	301	
Db	262	RTSCOPIPIVKLEWDSFWAVLPLAVVGIATLFWVTVFYNDTPVVKASGRELSSYL	321	
QY	302	LAGIFLCVATTFMLAEPLDGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS	361	
Db	322	LAGIFLCVATTFMLAEPLDGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS	381	
QY	362	APRFISPASQLAITFILISLQLLGLICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS	421	

Db 382 APRFISPAQLAITFILISLQLLGICVWFVDPSPSHVDFDQRTLDPRFARGVLKCDIS 441
Qy 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTS 481
Db 442 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTS 501
Qy 482 OSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPBQNPVKRSLKAVVTAATM 541
Db 502 OSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPBQNPVKRSLKAVVTAATM 561
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 584
Db 562 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 604

RESULT 2

PCT-US91-09422-19
; Sequence 19, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,806
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-6PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-09422-19

Query Match 98.2%; Score 3050.5; DB 5; Length 912;
Best Local Similarity 98.6%; Pred. No. 5.2e-300;
Matches 575; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
Qy 3 GVSSSLPRTMT-SGFDYFSSRTLNNRRNIWFAEFWEDNPHCKLSRHALKKGSHIKKCT 61
Db 330 GAVTILPKRMSVRGFDYFSSRTLNNRRNIWFAEFWEDNPHCKLSRHALKKGSHIKKCT 389

Qy 62 NRERIGODSAYEOBGKVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLKY 121
Db 390 NRERIGODSAYEOBGKVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLKY 449
Qy 122 IRNVNFSGIAGNPVTNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQWMP 181
Db 450 IRNVNFSGIAGNPVTNENGDAFGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERQWMP 509
Qy 182 GSGOQLPRSTCSLPQGERKKTVKGMACCMHCEPCTGYOYVDRTYCTKCPYDMRPTEN 241
Db 510 GSGOQLPRSTCSLPQGERKKTVKGMACCMHCEPCTGYOYVDRTYCTKCPYDMRPTEN 569
Qy 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGAATLFFVVVTFVRVYNDTPIVKASGRELSVVL 301
Db 570 RTSCQPIPIVKLEWDSWAVLPLFLAVVGAATLFFVVVTFVRVYNDTPIVKASGRELSVVL 629
Qy 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEGQKRSVS 361
Db 630 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEGQKRSVS 689
Qy 362 APRFISPAQLAITFILISLQLLGICVWFVDPSPSHVDFDQRTLDPRFARGVLKCDIS 421
Db 690 APRFISPAQLAITFILISLQLLGICVWFVDPSPSHVDFDQRTLDPRFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTS 481
Db 750 DLSLICLLGYSMMLMVTCTVVAIKTRGVPTFNEAKPIGFTMYTTCIWLAFIPFPGTS 809
Qy 482 OSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPBQNPVKRSLKAVVTAATM 541
Db 810 OSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPBQNPVKRSLKAVVTAATM 869
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 584
Db 870 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYVYTNHAI 912

RESULT 3

US-08-617-785-2
; Sequence 2, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Putner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-2

Query Match 96.7%; Score 3004.5; DB 3; Length 912;
Best Local Similarity 96.7%; Pred. No. 2.4e-295;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
Qy 3 GVSSSLPRTMT-SGFDYFSSRTLNNRRNIWFAEFWEDNPHCKLSRHALKKGSHIKKCT 61
Db 330 GAVTILPKRMSVRGFDYFSSRTLNNRRNIWFAEFWEDNPHCKLSRHALKKGSHIKKCT 389

Db 330 GAVTILPKRMSVRGFDYFSSRTLDNRRNIWPAEFWEDNFCKLSRHALKKGSHVKKCT 389
Qy 62 NRERIGQDSAYEQEGKQVFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 121
Db 390 NRERIGQDSAYEQEGKQVFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 449
Qy 122 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVGISWTDLHLRIERMOWP 181
Db 450 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVGISWTDLHLRIERMOWP 509
Qy 182 GSGQOLPRISICSLPCQGERKKTVMGMAACWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 241
Db 510 GSGQOLPRISICSLPCQGERKKTVMGMAACWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 569
Qy 242 RTSQOPIPIVKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTGCRPIPIKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 629
Qy 302 LAGIFLCVATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 630 LAGIFLCVATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689
Qy 362 APRFISPASQLAITFILISLQLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 421
Db 690 APRFISPASQLAITFILISLQLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMLLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIIVWLAFIPIFFGTS 481
Db 750 DLSLICLLGYSMLLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIIVWLAFIPIFFGTS 809
Qy 482 QSAOKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 541
Db 810 QSAOKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 869
Qy 542 SNKFTQKGNFRPNGEAKSELCELENLEPALATKQTYVTVYTNHAI 584
Db 870 SNKFTQKGNFRPNGEAKSELCELENLEPALATKQTYVTVYTNHAI 912

RESULT 4
US-09-641-318-2
; Sequence 2, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: GAYLO, PAUL J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756

TELEX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-641-318-2

Query Match 96.7%; Score 3004.5; DB 3; Length 912;
Best Local Similarity 96.7%; Pred. No. 2.4e-295;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
Qy 3 GVSSSLPRTMT-SGFDYFSSRTLDNRRNIWPAEFWEDNFCKLSRHALKKGSHVKKCT 61
Db 330 GAVTILPKRMSVRGFDYFSSRTLDNRRNIWPAEFWEDNFCKLSRHALKKGSHVKKCT 389
Qy 62 NRERIGQDSAYEQEGKQVFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 121
Db 390 NRERIGQDSAYEQEGKQVFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 449
Qy 122 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVGISWTDLHLRIERMOWP 181
Db 450 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVGISWTDLHLRIERMOWP 509
Qy 182 GSGQOLPRISICSLPCQGERKKTVMGMAACWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 241
Db 510 GSGQOLPRISICSLPCQGERKKTVMGMAACWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 569
Qy 242 RTSQOPIPIVKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTGCRPIPIKLEWDSWAVLPLFLAVVGIATLFFVVTTFVRYNDTPIVKASGRELSYVL 629
Qy 302 LAGIFLCVATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 630 LAGIFLCVATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689
Qy 362 APRFISPASQLAITFILISLQLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 421
Db 690 APRFISPASQLAITFILISLQLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMLLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIIVWLAFIPIFFGTS 481
Db 750 DLSLICLLGYSMLLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIIVWLAFIPIFFGTS 809
Qy 482 QSAOKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 541
Db 810 QSAOKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSUKAVVTAATM 869
Qy 542 SNKFTQKGNFRPNGEAKSELCELENLEPALATKQTYVTVYTNHAI 584
Db 870 SNKFTQKGNFRPNGEAKSELCELENLEPALATKQTYVTVYTNHAI 912

RESULT 5
US-09-817-464-2
; Sequence 2, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; HMR5, HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7

EARLIER FILING DATE: 1994-08-19
EARLIER APPLICATION NUMBER: EPO 93810663.0
EARLIER FILING DATE: 1993-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 912
TYPE: PRT
ORGANISM: Homo sapiens
US-09-817-464-2

Query Match 96.7%; Score 3004.5; DB 4; Length 912;
Best Local Similarity 96.7%; Pred. No. 2.46-295;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

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Qy 3 GVSSSLPRTMT-SGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 330 GAVTILPKRMSVRGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHVKKCT 389
Qy 62 NRERIGDSAYEQQGKQVFVDVAYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLKY 121
Db 390 NRERIGDSAYEQQGKQVFVDVAYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLKY 449
Qy 122 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVIKSWTDHLHLRIERQWP 181
Db 450 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVIKSWTDHLHLRIERQWP 509
Qy 182 GSGQQLPRISCSLPCQGERKKTVMKMACWHCEPCTGYQYQVDRYCTKTCPYDMRPTEN 241
Db 510 GSGQQLPRISCSLPCQGERKKTVMKMACWHCEPCTGYQYQVDRYCTKTCPYDMRPTEN 569
Qy 242 RTSQCPPIVKLEWDSWAVLPLFLAVVGGIAATLFFVVTTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTGCRPIIILKLEWDSWAVLPLFLAVVGGIAATLFFVVTTFVRYNDTPIVKASGRELSYVL 629
Qy 302 LAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS 361
Db 630 LAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS 689
Qy 362 APRISPASOLAITFILISLQLLGCICWFFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db 690 APRISPASOLAITFILISLQLLGCICWFFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 749
Qy 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIWLAFIPFFGTS 481
Db 750 DLSLICLLGYSMMLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIWLAFIPFFGTS 809
Qy 482 QSAQKLYIQTTLTVSVSLSASVSLGMLYMPKVYIILFHPQNPVKRKSILKAVVTAATM 541
Db 810 QSAQKLYIQTTLTVSVSLSASVSLGMLYMPKVYIILFHPQNPVKRKSILKAVVTAATM 869
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 870 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 912
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RESULT 6

US-08-855-146-2
Sequence 2, Application US/08855146
Patent No. 6221609
GENERAL INFORMATION:
APPLICANT: Belagaje, Rama M.
APPLICANT: Wu, Su
TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
NUMBER OF INVENTIONS: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Department
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,146
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,243
FILING DATE: 07-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-10836
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-6334
TELEFAX: (317) 276-2764
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-855-146-2

Query Match 76.3%; Score 2370; DB 3; Length 908;

Best Local Similarity 75.0%; Pred. No. 5.5e-231;
Matches 437; Conservative 58; Mismatches 86; Indels 2; Gaps 2;

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Qy 3 GVSSSLPRTMT-SGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 327 GAVTILPKRASIDGDFRYSRTLDNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 385
Qy 62 NRERIGDSAYEQQGKQVFVDVAYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLKY 121
Db 386 GLERIASDSSVEQEGKQVFVDVAYSMAYALHNNHKKDLCPCYIGLCPRMSTIDGKELGY 445
Qy 122 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVIKSWTDHLHLRIERQWP 181
Db 446 IRNVNFSGIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKVIKSWTDHLHLRIERQWP 505
Qy 182 GSGQQLPRISCSLPCQGERKKTVMKMACWHCEPCTGYQYQVDRYCTKTCPYDMRPTEN 241
Db 506 HRETHPASVCSLPCQGERKKTVMKMACWHCEPCTGYQYQVDRYCTKTCPYDMRPTEN 565
Qy 242 RTSQCPPIVKLEWDSWAVLPLFLAVVGGIAATLFFVVTTFVRYNDTPIVKASGRELSYVL 301
Db 566 RTGCOLIPIIKLEWDSWAVLPLFLAVVGGIAATLFFVVTTFVRYNDTPIVKASGRELSYVL 625
Qy 302 LAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKTNRIYRIFEQKRSVS 361
Db 626 LTGIFLCYSITFLMIAAPDTIICSFRRVFLGLGMSISYAALLTKTNRIYRIFEQKRSVS 685
Qy 362 APRISPASOLAITFILISLQLLGCICWFFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 421
Db 686 APRISPASOLAITFILISLQLLGCICWFFVVDPSHVVDFODQRTLDRPFARGVLKCDIS 745
Qy 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIWLAFIPFFGTS 481
Db 746 DLSLICLLGYSMMLMVTCTVYAIKTRGVPETFNPAKPIGFTMYTTCIWLAFIPFFGTS 805
Qy 482 QSAQKLYIQTTLTVSVSLSASVSLGMLYMPKVYIILFHPQNPVKRKSILKAVVTAATM 541
Db 806 QSAQKLYIQTTLTVSVSLSASVSLGMLYMPKVYIILFHPQNPVKRKSILKAVVTAATM 865
Qy 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 866 QSKLIQKGNDRPNGEAKSELCELENLETPALATKQTYVYTNHAI 908
```

RESULT 7

US-08-823-110-1
; Sequence 1, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-823-110-1
Query Match 74.9%; Score 2328; DB 3; Length 908;
Best Local Similarity 76.0%; Pred. No. 1e-226;
Matches 430; Conservative 53; Mismatches 81; Indels 2; Gaps 2;
QY 3 GVSSSLPRMT-SGDRVPSRTLDNRRNINWFAEFMEDNFCKLSRLHKKGSHKKCT 61
DB 327 GAVTILPKRASIDGDFRFRSRTLANNRNVWFAEFWEENFGCKLGSHG-KRNSHKKCT 385
QY 62 NRERIGQDSAYEQEGKVQFVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTOLKLY 121
DB 386 GLERARUSSVEQEGKVQFVIDAVYSMAYALHNMHKLCPGVIGLCPRMSTIDGKELGY 445
QY 122 IRNVNFGSIAGNPVTTFNENGAPGRYDIYQYQLRNGSABYKVGISWTDHLHLRIERMOWP 181
DB 446 IRNVNFGSAGTPTTFNENGAPGRYDIYQYQLRNGSABYKVGISWTDHLHLRIERMOWP 505
QY 182 GSGQQLPRISICLPQGRKKTVMACCHCECTGYQYQVDRTCTCTCPYDMRPTE 241
DB 506 HREHTHPASVCLPCKPGRKKTVMACCHCECTGYQYQVDRTCTCTCPYDMRPTE 565
QY 242 RTSCQPIPIVKLEWSPNAVLPLFVAVVGIATLFWVTFVRYNDTPIVKASGRELSVYL 301
DB 566 RTGCOLIPIIKLEWSPNAVLPLFVAVVGIATLFWVTFVRYNDTPIVKASGRELSVYL 625

QY 302 LAGIFLCYATTFMTAEPLDGLTCSIRIFLGLGMSISYAALLTKTNRIYRIFEOGRKSVS 361
DB 626 LTGIFLCYSITFLMIAADPTTICSFRRVFLGLGMCFSYAALLTKTNRIYRIFEOGRKSVT 685
QY 362 APRFISPASQAIATFILISLQLLGICVWFVVDPSHSVVDFODQRTLDPRFARGVLKCDIS 421
DB 686 APKFTISPASQVITFSLISVQLLGCVWFVVDPPHIIIDYGEQRTLDPEKARGVLKCDIS 745
QY 422 DLSLICLLGYSNLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIWLAPIPFGTS 481
DB 746 DLSLICSLGYSILLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIWLAPIPFGTA 805
QY 482 QSAKGLYIQTTLTVSVLSASVSIGMLYMPKVYIILPHBQNVKRSKAVVTAATM 541
DB 806 QSAKMYIQTTLTVSMLSASVSIGMLYMPKVYIILPHBQNVKRSKAVVTAATM 865
QY 542 SNKFTQKGNFRPNGEAKSELCELET 567
DB 866 QSKLIQKGNDRPNGEVKSCELET 891

RESULT 8
US-08-604-298-1
; Sequence 1, Application US/08604298
; Patent No. 6084084
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,298
; FILING DATE: February 21, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-604-298-1
Query Match 74.9%; Score 2328; DB 3; Length 908;
Best Local Similarity 76.0%; Pred. No. 1e-226;

Matches	430;	Conservative	53;	Mismatches	81;	Indels	2;	Gaps	2;
Qy	3	GVSSSLPRTMT-SGFDYFSSRTLDNRRNIIWFAEFWEDNFHCKLSRHALKGSHIKKCT	61	:	:	:	:	:	:
Db	327	GAVTILPKRASIDGFDYFRSRTLANRRNVWFAEFWEEFGCKLGSHG-KRNSHIKKCT	385	:	:	:	:	:	:
Qy	62	NRIRIGDSAYEQEGKVQFVIDAVYANGHALHAMHRDLCGRVGLCPRMPDVGDTQLLK	121	:	:	:	:	:	:
Db	386	GLERIAARDSYEQEGKVQFVIDAVYSMAYALHNNHKDLCFGYILGCPRMSTIDGKELGY	445	:	:	:	:	:	:
Qy	122	IRNVNFGSIGAGNPVTFNENGADPGRYDIYOQLRANGSAEYKVIQSWTDLHLRLRERMOWP	181	:	:	:	:	:	:
Db	446	IRAVNFGSAGTPVTFNENGADPGRYDIFQIITNKSTEVKVIQGHWTNQLHLKVEDNQWA	505	:	:	:	:	:	:
Qy	182	GSQQLPERSICSLPCQPERKKTVKGMACCMHCEPCTGYOQVDRYTCKTCPYDMRPTEN	241	:	:	:	:	:	:
Db	506	HREHTHPASVCSLPCPKGERKKTVKGVPCWCHCERCERYNQVDELSCELCPDQRPNNM	565	:	:	:	:	:	:
Qy	242	RTSCQPTPIVKLEHDSPAWVLPFLAVVGTAATLFFVVTFRYNDTPIVKASGRELSYVL	301	:	:	:	:	:	:
Db	566	RTGQLPIPIKLEHSPWAVPVPAVLGIATTFVITFVRYNDTPIVRASGRELSYVL	625	:	:	:	:	:	:
Qy	302	LAGIFLCVATTFMLIASPDLGTCSLRIFIFLGLGMSISVAALLTKTNRIYRIFEOGKRSVS	361	:	:	:	:	:	:
Db	626	LTGIFLCYSITFLMIAPDTIICSFRVFFLGLGNCFPFYAALLTKTNRIHRIFEOGKKSVT	685	:	:	:	:	:	:
Qy	362	APRFIPASQIAITFIILISQLLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS	421	:	:	:	:	:	:
Db	686	APKFPISASQLVITFSLISVQLLGIVFVWFVVDPPHIIIDYGEQRTLDPEKARGVLKCDIS	745	:	:	:	:	:	:
Qy	422	DLSLILCLLGSMLLMWCTVVAIKTRGVPEFNEAKPIGFTMYTTCILWLAFTPIPRGTS	481	:	:	:	:	:	:
Db	746	DLSLICLSLGSILMLMVCTVVAIKTRGVPEFNEAKPIGFTMYTTCILWLAFTPIPRGTA	805	:	:	:	:	:	:
Qy	482	QSAKLIYQITTLTVSVSLSASVSLGMLYMPKVIIILFHPHEQNVPKRSLKAVVTAATM	541	:	:	:	:	:	:
Db	806	QSAEKWYIQITTLTVSNLSLSASVSLGMLYMPKVIIILFHPHEQNVQKRSEKAVVTAATM	865	:	:	:	:	:	:
Qy	542	SNKPTQKGNFRPNGEAKSELCEINLET	567	:	:	:	:	:	:
Db	866	QSKLIOKGNDRPNGEAKSELCESET	891	:	:	:	:	:	:

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RESULT 9
US-08-617-785-12
; Sequence 12, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; TITLE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-12

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Best Local Similarity 69.9%; Pred. No. 1.2e-215; Matches 408; Conservative 74; Mismatches 100; Indels 2; Gaps 2;	
Qy	3 GVSSSPTRMT-SGFDRYSSRRLDNNRRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 61
Db	332 GAITIQKRAIVEGEDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKKEDTORCKT 391
Qy	62 NRRIIGODSAYBOEGKVQFVIDAVYANGHALHAMRDLCPGRVGLCPMDPVDGCTOLLKY 121
Db	392 GOERIGKDSYBOEGKVQFVIDAVYAMAHAMHNKDLCADYRGVCPMEQAGGKLLKY 451
Qy	122 IRNVNFGSIAGNPVTNFNENGDAGRYDIYQYQLRNGS-AEYKIVIGSWTIDHLHLRIERMOW 180
Db	452 IRNVNFGSAGTPVMFNKNGDAGRYDIYFOYQTNTSNPCYRLIGQWTDDELQNLNEDMQW 511
Qy	181 PGSGOQLPRSICSLPCQPGBERKTVTGMACCWHCEBCTGYQYQVDRTYCTKTCPYDMRPTE 240
Db	512 GKGVEITPASVCTLPCKPGQKKTKQGTGTCPCWCEPCDGYQYQFDEMTQCHCPYDQRPNE 571
Qy	241 NRTSCQPIPTVKLEWDSPAVLPLFLAVVGIAATLFWVTFRVYNDTPTVKASGRELSYV 300
Db	572 NRTGCCQDPIIKLEWSPNAVIVPFLAMLGLIATIFVMATFRYNDTPIVRASGRELSYV 631
Qy	301 LLAGIFLCYATTPLMIABDPLGTCSSRRIFPLGLGMSISYAALLTKTNRIYRIFEQGKRSV 360
Db	632 LLTGIFLCYITITELMIAKPDVAVCSFRRVFLGLGMCISYAALLTKTNRIYRIFEQGKKS 691
Qy	361 SARFETSPASQLAITFLTSLQLLGHCVWFVDPDPSHVDFODORTLDRPFARGVLKCDI 420
Db	692 TAPRLISPTSLAITSSLSISVQLLGVPWFVGDPPNIIIDYDEHKTWNPEQARGVLKCDI 751
Qy	421 SDLSLICLLGYSMLLMVTCVYAIKTRGVPTETNEAKPIGFTMYTTCI VWLAPIPIFFGT 480
Db	752 TDLQIICSLGYSILLMVTCVYAIKTRGVPTENFEAKPIGFTMYTTCI VWLAPIPIFFGT 811
Qy	481 SQSADKLYIOTTTTLTVSVSLSASVSGMLYMPKVYIILFHPPEONVPRKRSKAVVTAAT 540
Db	812 AQSAEKYIOTTTTLTSMNLUSASVALGMLYMPKVYIILFHPPELVQKRKRSKAVVTAAT 871
Qy	541 MSNKFTQKGNFRPNGEAKSELCSLENLETPALATKQTYVTYTNHAI 584
Db	872 MSRLSHKPSDRPNGEAKTELCENVDPNSPAAKKKTVSYNNLVI 915

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RESULT 10
US-09-817-464-12
; Sequence 12, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCES: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-464-12

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Query Match 71.4%; Score 2219; DB 4; Length 915;
Best Local Similarity 69.9%; Pred. No. 1.2e-215;
Matches 408; Conservative 74; Mismatches 100; Indels 2; Gaps 2;

QY 3 GVSSSLPTMT-SGPDYFSSRTLNNRRNIWFAEFWEDNFHCKLSRHAKKGSHIKCT 61
Db 332 GAITIQPKATVEGDFAYFTSRTLENNRRNVFAEYWEENFNCKLTISSGKEDTRKCT 391
QY 62 NRERIGQDSAYEQEGKQVQVIDAVYAMGHALHAMRDLCPCRGVGLCPRMDPVDGTQLLKY 121
Db 392 QGERIGKDSNYEQEGKQVQVIDAVYAMAHALHNNKDLCADYRGVCPMEQAGGKLLKY 451
QY 122 IRNVNFGSIAGNVTFFNENGDPGRYDIYQYQLRNGS-AEYKIVGSWTDHLHLRTERMQW 180
Db 452 IRNVNFGSAGTPVMFNKNGDPGRYDIYQYQTTNTNSPGYRLIGQWTDLQNLNEDMQW 511
QY 181 PGSGQOLPRISCSLPCQGERKTKVGMACWHCEPCTGYQYQVDRYTCKTCPYDMRPT 240
Db 512 KGKVEIPASVCTLCKPQQRKTKQKTPCCWTCPCDGYQYQFDEMTQCHCPYQORPNE 571
QY 241 NRTSQPIPIVKLEWDSMAVLPFLAVVGGIAATLFFVVVTFVRYNDTPIVKAAGRELSYV 300
Db 572 NRTGQDPIIKLEWHSMAVLPFLAVVGGIAATLFFVMAATFIRYNDTPIVRASGRELSYV 631
QY 301 LLAGIFLCYATTFMLIAEPDLGTSRLRIFLGLGMSISYAAALLTKNRIYRIFEGQKRSV 360
Db 632 LLTGIFLCYIITFLMIAKPDVAVCSFRFVFLGLGMCISYAAALLTKNRIYRIFEGQKRSV 691
QY 361 SAPRISPASOLAITFILISLQLLGICVWFVVDPSHSVVDFOQRTLDPRFARGVLKCDI 420
Db 692 TAPRLISPTSQALITSSLSVQLLGVIWFGVDPNNIIDIYDEHKTMPQEQARGVLKCDI 751
QY 421 SDLSLICLLGYSLMLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFFT 480
Db 752 TDLQIICSLGYSLMLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFFT 811
QY 481 SOSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPKRKSUKAVVTAAT 540
Db 812 AQSAEKLYIQTTLTISMLNSASVALGMLYMPKVYIILFHPBELNVQKRKSPKAVVTAAT 871
QY 541 MSNKFTQGNFRPNRNGEAKSELCELETALATKQYVTVYTNHAI 584
Db 872 MSSRLSHKPSDRPNRNGEAKTELCELVDPNSPAKKKYVSNNLVI 915
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RESULT 11

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US-08-453-862-2
; Sequence 2, Application US/08453862
; Patent No. 5738999
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,862
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 436
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-453-862-2

Query Match 71.1%; Score 2210; DB 1; Length 915;
Best Local Similarity 69.5%; Pred. No. 9.5e-215;
Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

QY 3 GVSSSLPTMT-SGPDYFSSRTLNNRRNIWFAEFWEDNFHCKLSRHAKKGSHIKCT 61
Db 332 GAITIQPKATVEGDFAYFTSRTLENNRRNVFAEYWEENFNCKLTISSGKEDTRKCT 391
QY 62 NRERIGQDSAYEQEGKQVQVIDAVYAMGHALHAMRDLCPCRGVGLCPRMDPVDGTQLLKY 121
Db 392 QGERIGKDSNYEQEGKQVQVIDAVYAMAHALHNNKDLCADYRGVCPMEQAGGKLLKY 451
QY 122 IRNVNFGSIAGNVTFFNENGDPGRYDIYQYQLRNGS-AEYKIVGSWTDHLHLRTERMQW 180
Db 452 IRNVNFGSAGTPVMFNKNGDPGRYDIYQYQTTNTNPYRLIGQWTDLQNLNEDMQW 511
QY 181 PGSGQOLPRISCSLPCQGERKTKVGMACWHCEPCTGYQYQVDRYTCKTCPYDMRPT 240
Db 512 KGKVEIPSSVCTLCKPQQRKTKQKTPCCWTCPCDGYQYQFDEMTQCHCPYQORPNE 571
QY 241 NRTSQPIPIVKLEWDSMAVLPFLAVVGGIAATLFFVVVTFVRYNDTPIVKAAGRELSYV 300
Db 572 NRTGQDPIIKLEWHSMAVLPFLAVVGGIAATLFFVMAATFIRYNDTPIVRASGRELSYV 631
QY 301 LLAGIFLCYATTFMLIAEPDLGTSRLRIFLGLGMSISYAAALLTKNRIYRIFEGQKRSV 360
Db 632 LLTGIFLCYIITFLMIAKPDVAVCSFRFVFLGLGMCISYAAALLTKNRIYRIFEGQKRSV 691
QY 361 SAPRISPASOLAITFILISLQLLGICVWFVVDPSHSVVDFOQRTLDPRFARGVLKCDI 420
Db 692 TAPRLISPTSQALITSSLSVQLLGVIWFGVDPNNIIDIYDEHKTMPQEQARGVLKCDI 751
QY 421 SDLSLICLLGYSLMLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFFT 480
Db 752 TDLQIICSLGYSLMLMVTCTVYAIKTRGVPEFNEAKPIGFTMYTTCIVWLAFIPIFFT 811
QY 481 SOSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPKRKSUKAVVTAAT 540
Db 812 AQSAEKLYIQTTLTISMLNSASVALGMLYMPKVYIILFHPBELNVQKRKSPKAVVTAAT 871
QY 541 MSNKFTQGNFRPNRNGEAKSELCELETALATKQYVTVYTNHAI 584
Db 872 MSSRLSHKPSDRPNRNGEAKTELCELVDPNSPAKKKYVSNNLVI 915

RESULT 12
US-08-452-734A-2
; Sequence 2, Application US/08452734A
; Patent No. 5831047
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
```

```

; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/452,734A
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-452-734A-2

Query Match 71.1%; Score 2210; DB 2; Length 915;
Best Local Similarity 69.5%; Pred. No. 9.5e-215;
Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

Qy 3 GVSSSLPRTMT-SGFDRYFSSRTLDNNRRNWFAPFWEEDNPHCKLSRHALKKGSHIKKCT 61
Db 332 GAITIQKRAIVGFDAYFTSRTLENNRRNWFAYEENFNCKLTISGSKKEDTRKCT 391
Qy 62 NRERIGQDSAYEQGKQVFVIDAVYAMGHALHAMHRLDCPGRVGLCPRMDPVDGTLLKY 121
Db 392 GQERIGKDSNYEQGKQVFVIDAVYAMAHALHMHKDLCADYRGVCPMEQAGGKLLKY 451
Qy 122 IRNVNFGIAGNPVTFNENGDAFGRYDIYQYQLRN-GSAEYKVGISWTDHLHLRIERMOW 180
Db 452 IRHVNFGSAGTPWFNKNKGDAFGRYDIYQYQLRN-GSAEYKVGISWTDHLHLRIERMOW 511
Qy 181 PGSQQLPRISCPLCPQGERKKTVMGACWCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
Db 512 GKVREIPSSVCTLPCKPQGRKTKQKTPCWTCEPCDGYQYQVDEMTCQHCYDQRPNE 571
Qy 241 NRTSCQPIPIVKLEWSPWAVLFLAVVGIAATFLFVVVTFVRYNDTPPIVKASGRELSYV 300
Db 572 NRTGQNIPIIKLEWSPWAVIPVFLMLGIATIFVMAITFIYNDTPPIVRAASGRELSYV 631
Qy 301 LLAGIFLCYATTFMLIAEPDGLTCSLRIIFLGLGMSISYAALLTKNRIYRIFPQGRSV 360
Db 632 LITGIFLCYIITFLMIAPDVAVCSFRVFLGLGMCISYAALLTKNRIYRIFPQGRSV 691
Qy 361 SAPRFISPAQLAITFILISLQLGICVWFVVDPSHVSVDQDQRTLDPRFARGVLKCDI 420
Db 692 TAPRLISPTSQLAITSSLSVQLLVGFVFWGVDPPNIIIDYDEHKTWNPEQARGVLKCDI 751
Qy 421 SDSLICLLGYSMLLMVTCTYAIKTRGVPTFNEAKPIGFTMTTTCIVWLAFIPFPGT 480
Db 752 TDLOIICSLGYSILLMVTCTYAIKTRGVPTFNEAKPIGFTMTTTCIVWLAFIPFPGT 811
Qy 481 QSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPHQNVKPKRSLKAVVTAAT 540

; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/452,734A
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-452-734A-2

Query Match 71.1%; Score 2210; DB 3; Length 915;
Best Local Similarity 69.5%; Pred. No. 9.5e-215;
Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

Qy 3 GVSSSLPRTMT-SGFDRYFSSRTLDNNRRNWFAPFWEEDNPHCKLSRHALKKGSHIKKCT 61
Db 332 GAITIQKRAIVGFDAYFTSRTLENNRRNWFAYEENFNCKLTISGSKKEDTRKCT 391
Qy 62 NRERIGQDSAYEQGKQVFVIDAVYAMGHALHAMHRLDCPGRVGLCPRMDPVDGTLLKY 121
Db 392 GQERIGKDSNYEQGKQVFVIDAVYAMAHALHMHKDLCADYRGVCPMEQAGGKLLKY 451
Qy 122 IRNVNFGIAGNPVTFNENGDAFGRYDIYQYQLRN-GSAEYKVGISWTDHLHLRIERMOW 180
Db 452 IRHVNFGSAGTPWFNKNKGDAFGRYDIYQYQLRN-GSAEYKVGISWTDHLHLRIERMOW 511
Qy 181 PGSQQLPRISCPLCPQGERKKTVMGACWCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
Db 512 GKVREIPSSVCTLPCKPQGRKTKQKTPCWTCEPCDGYQYQVDEMTCQHCYDQRPNE 571
Qy 241 NRTSCQPIPIVKLEWSPWAVLFLAVVGIAATFLFVVVTFVRYNDTPPIVKASGRELSYV 300
Db 572 NRTGQNIPIIKLEWSPWAVIPVFLMLGIATIFVMAITFIYNDTPPIVRAASGRELSYV 631
Qy 301 LLAGIFLCYATTFMLIAEPDGLTCSLRIIFLGLGMSISYAALLTKNRIYRIFPQGRSV 360
Db 632 LITGIFLCYIITFLMIAPDVAVCSFRVFLGLGMCISYAALLTKNRIYRIFPQGRSV 691
Qy 361 SAPRFISPAQLAITFILISLQLGICVWFVVDPSHVSVDQDQRTLDPRFARGVLKCDI 420
Db 692 TAPRLISPTSQLAITSSLSVQLLVGFVFWGVDPPNIIIDYDEHKTWNPEQARGVLKCDI 751
Qy 421 SDSLICLLGYSMLLMVTCTYAIKTRGVPTFNEAKPIGFTMTTTCIVWLAFIPFPGT 480
Db 752 TDLOIICSLGYSILLMVTCTYAIKTRGVPTFNEAKPIGFTMTTTCIVWLAFIPFPGT 811
Qy 481 QSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPHQNVKPKRSLKAVVTAAT 540

; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/176,401B
; FILING DATE: 30-DECEMBER-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-401B-2

Query Match 71.1%; Score 2210; DB 3; Length 915;
Best Local Similarity 69.5%; Pred. No. 9.5e-215;
Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

Qy 3 GVSSSLPRTMT-SGFDRYFSSRTLDNNRRNWFAPFWEEDNPHCKLSRHALKKGSHIKKCT 61
Db 332 GAITIQKRAIVGFDAYFTSRTLENNRRNWFAYEENFNCKLTISGSKKEDTRKCT 391
Qy 62 NRERIGQDSAYEQGKQVFVIDAVYAMGHALHAMHRLDCPGRVGLCPRMDPVDGTLLKY 121
Db 392 GQERIGKDSNYEQGKQVFVIDAVYAMAHALHMHKDLCADYRGVCPMEQAGGKLLKY 451
Qy 122 IRNVNFGIAGNPVTFNENGDAFGRYDIYQYQLRN-GSAEYKVGISWTDHLHLRIERMOW 180
Db 452 IRHVNFGSAGTPWFNKNKGDAFGRYDIYQYQLRN-GSAEYKVGISWTDHLHLRIERMOW 511
Qy 181 PGSQQLPRISCPLCPQGERKKTVMGACWCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
Db 512 GKVREIPSSVCTLPCKPQGRKTKQKTPCWTCEPCDGYQYQVDEMTCQHCYDQRPNE 571
Qy 241 NRTSCQPIPIVKLEWSPWAVLFLAVVGIAATFLFVVVTFVRYNDTPPIVKASGRELSYV 300
Db 572 NRTGQNIPIIKLEWSPWAVIPVFLMLGIATIFVMAITFIYNDTPPIVRAASGRELSYV 631
Qy 301 LLAGIFLCYATTFMLIAEPDGLTCSLRIIFLGLGMSISYAALLTKNRIYRIFPQGRSV 360
Db 632 LITGIFLCYIITFLMIAPDVAVCSFRVFLGLGMCISYAALLTKNRIYRIFPQGRSV 691
Qy 361 SAPRFISPAQLAITFILISLQLGICVWFVVDPSHVSVDQDQRTLDPRFARGVLKCDI 420
Db 692 TAPRLISPTSQLAITSSLSVQLLVGFVFWGVDPPNIIIDYDEHKTWNPEQARGVLKCDI 751
Qy 421 SDSLICLLGYSMLLMVTCTYAIKTRGVPTFNEAKPIGFTMTTTCIVWLAFIPFPGT 480
Db 752 TDLOIICSLGYSILLMVTCTYAIKTRGVPTFNEAKPIGFTMTTTCIVWLAFIPFPGT 811
Qy 481 QSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPHQNVKPKRSLKAVVTAAT 540
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Db 572 NRTGCONIPIIKLEWHSPWAVIPVFLMGLIATIFVWATFIRYNDTPIVRASGRELSTV 631
Qy 301 LLAGIFLCYATTFLMIAEPDLGTSRLRIFLGLGMSISYAAALLTKTNRIYRIFEOGKRSV 360
Db 632 LLTGIFLCYIITFLMIAKPDVAVCSFRVFLGLGMCISYAAALLTKTNRIYRIFEOGKRSV 691
Qy 361 SAPRISPASQAIATFILLISQLLIGICWVVDPSHVSVDFOQRTLPDRFARGVLKCDI 420
Db 692 TAPRLISPTSQAIATSSLSISVQLLGVFIWFGVDPENIIIDYDEHKTMNPEQARGVLKCDI 751
Qy 421 SDLSILICLLGYSMLLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIWLAFIPIFGT 480
Db 752 TDLQIICSLGYSILLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIWLAFIPIFGT 811
Qy 481 SOSADKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPBQNVPKRKSILKAVVTAAT 540
Db 812 AQSACKLYIQTTLTISNLSASVALGMLYMPKVYIILFHPBQNVPKRKSILKAVVTAAT 871
Qy 541 MSNKPTQGNFRPNGEAKSELCELENLETALATKQTYVYTNHAI 584
Db 872 MSSRLSHKPSDRPNGEAKTELCENVDPNSPAACKKYVSNNLVI 915

RESULT 14

PCT-US94-14989-2

; Sequence 2, Application PC/TUS9414989

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS

; NUMBER OF SEQUENCES: 3

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; PCT APPLICATION NUMBER: PCT/US94/14989

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/176,401

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCE/DOCKET NUMBER: 13952-18PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 467-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 915 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-14989-2

Query Match 71.1%; Score 2210; DB 5; Length 915;

Best Local Similarity 69.5%; Pred. No. 9.5e-215;

Matches 406; Conservative 76; Mismatches 100; Indels 2; Gaps 2;

Qy 3 GVSSSLPRMT-SGPDYFSSRTLNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 332 GAITIQKRAIVEGFDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKEDTDKCT 391
Qy 62 NREIRGQDSAYEQSGKQVFDIVAYMGHALHAMHRDLCPRVGLCPDMPVDGTQLLY 121
Db 392 GQERIGKDSNVEQSGKQVFDIVAYMAHALHMKDLKADYRGVCPMEQAGGKLLKY 451
Qy 122 IRNVNFGIAGNPVTFNENGDPGRYDIYQQLRNGS-AEYKVIGSWTDHLHLRIERMOW 180
Db 452 IRNVNFGSAGTPTVMFNKNGDAPGRYDIFQYOTTNTNPGYRLIGQWTDLQNLIEDMOW 511

Qy 191 PGSGOOLPRISCSLPQCPGERKKTVMGMACCWHCEPCTGYQVQDRTYCKTCYDMRPT 240
Db 512 GKGVEIPESSVCTLPCKPQQRKTKQKTPCCWTCPCDGYQYQFDEMTCQHCPCYDQRPNE 571
Qy 241 NRTSCOPTPIVKLEWDSMAVLPLFLAVVGTAAATLPVVVTFVRYNDTPIVKASGRELSTV 300
Db 572 NRTGCONIPIIKLEWHSPWAVIPVFLMGLIATIFVWATFIRYNDTPIVRASGRELSTV 631
Qy 301 LLAGIFLCYATTFLMIAEPDLGTSRLRIFLGLGMSISYAAALLTKTNRIYRIFEOGKRSV 360
Db 632 LLTGIFLCYIITFLMIAKPDVAVCSFRVFLGLGMCISYAAALLTKTNRIYRIFEOGKRSV 691
Qy 361 SAPRISPASQAIATFILLISQLLIGICWVVDPSHVSVDFOQRTLPDRFARGVLKCDI 420
Db 692 TAPRLISPTSQAIATSSLSISVQLLGVFIWFGVDPENIIIDYDEHKTMNPEQARGVLKCDI 751
Qy 421 SDLSILICLLGYSMLLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIWLAFIPIFGT 480
Db 752 TDLQIICSLGYSILLMVTCVYAIKTRGVPEFNEAKPIGFTMYTTCIWLAFIPIFGT 811
Qy 481 SOSADKLYIQTTLTIVSVLSASVSLGMLYMPKVYIILFHPBQNVPKRKSILKAVVTAAT 540
Db 812 AQSACKLYIQTTLTISNLSASVALGMLYMPKVYIILFHPBQNVPKRKSILKAVVTAAT 871
Qy 541 MSNKPTQGNFRPNGEAKSELCELENLETALATKQTYVYTNHAI 584
Db 872 MSSRLSHKPSDRPNGEAKTELCENVDPNSPAACKKYVSNNLVI 915

RESULT 15

US-08-617-785-4

; Sequence 4, Application US/08617785E

; Patent No. 6228610

; GENERAL INFORMATION:

; APPLICANT: Flor, Peter J.

; APPLICANT: Kuhn, Ranier

; APPLICANT: Lindaur, Kristen

; APPLICANT: Knopfel, Irene

; APPLICANT: Thomas

; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,

; FILE REFERENCE: 4-19679/A/PCT

; CURRENT APPLICATION NUMBER: US/08/617,785E

; CURRENT FILING DATE: 1996-03-19

; EARLIER APPLICATION NUMBER: PCT/EP94/02991

; EARLIER FILING DATE: 1994-09-07

; EARLIER APPLICATION NUMBER: EPO 9416553.7

; EARLIER FILING DATE: 1994-08-19

; EARLIER APPLICATION NUMBER: EPO 93810663.0

; EARLIER FILING DATE: 1993-09-20

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 4

; LENGTH: 867

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-617-785-4

Query Match 70.5%; Score 2191.5; DB 3; Length 867;

Best Local Similarity 69.3%; Pred. No. 6.6e-213;

Matches 405; Conservative 73; Mismatches 99; Indels 7; Gaps 3;

Qy 3 GVSSSLPRMT-SGPDYFSSRTLNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 277 GAITIQKRAIVEGFDAYFTSRTLENNRRNVFAEYWEENFNCKLTISGSKEDTDKCT 336
Qy 62 NREIRGQDSAYEQSGKQVFDIVAYMGHALHAMHRDLCPRVGLCPDMPVDGTQLLY 121
Db 337 GQERIGKDSNVEQSGKQVFDIVAYMAHALHMKDLKADYRGVCPMEQAGGKLLKY 396
Qy 122 IRNVNFGIAGNPVTFNENGDPGRYDIYQQLRNGS-AEYKVIGSWTDHLHLRIERMOW 180
Db 397 IRNVNFGSAGTPTVMFNKNGDAPGRYDIFQYOTTNTNPGYRLIGQWTDLQNLIEDMOW 456

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2005, 17:59:08 ; Search time 165 Seconds
(without alignments)
1368.897 Million cell updates/sec

Title: US-10-828-332-7

Perfect score: 3107

Sequence: 1 MPGVSSLPRTMTSGFDRYF.....LETPALATKQTVYVYTHAI 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3107	100.0	584	ABR56244	Rat gluta
2	3050.5	98.2	604	ABG74133	Rat metab
3	3050.5	98.2	912	ABG74133	Rat Prote
4	3050.5	98.2	912	ABG74133	Rat Prote
5	3017	97.1	909	ADO29095	Mouse nov
6	3004.5	96.7	909	AAOI15101	Human pns
7	3004.5	96.7	912	AAE23757	Human met
8	3004.5	96.7	912	AAE23757	Human met
9	3004.5	96.7	912	ABP81846	Human met
10	3004.5	96.7	912	ABP81846	Human met
11	3004.5	96.7	912	ABP81846	Human pro
12	3004.5	96.7	912	ADO29094	Human nov
13	3004.5	96.7	912	ADO29094	Human nov
14	3001.5	96.6	912	AAQ89114	Human uro
15	2912.5	93.7	591	AAQ89114	Human pro
16	2852.5	91.8	886	ABM84666	Human dia
17	2719	87.5	796	ADRL0452	Human pro
18	2713	87.3	862	ABM84667	Human dia
19	2710.5	87.2	1422	AAOI15102	Human phm
20	2377	76.5	908	ABR62488	Human met
21	2377	76.5	908	ABR62489	Human met
22	2377	76.5	908	ADO29476	Human met
23	2374	76.4	908	ABR62490	Human met
24	2370	76.3	908	AAW41568	Human met
25	2370	76.3	908	ABB09564	Human GRM

26	2370	76.3	908	6	ABP81850	Human met
27	2370	76.3	908	7	ADE31729	Human 255
28	2370	76.3	908	8	ADQ89128	Human uro
29	2369	76.2	908	6	ABR62491	Human met
30	2348	75.6	1142	4	ABG29451	Novel hum
31	2336	75.2	908	8	ADO29477	Mouse GPC
32	2328	74.9	908	2	AAW49928	Human met
33	2328	74.9	913	4	ABG29452	Novel hum
34	2219	71.4	915	5	ABG95155	Human GPC
35	2219	71.4	915	6	ABP81849	Human met
36	2219	71.4	915	7	ABE55969	Human pro
37	2219	71.4	915	7	ADJ93191	Human met
38	2219	71.4	915	8	ADO29103	Human nov
39	2215	71.3	915	2	AAQ72097	Human met
40	2214	71.3	915	5	ABG95164	Human GPC
41	2214	71.3	915	8	ADO29104	Mouse nov
42	2213	71.2	915	5	ABG95165	Human GPC
43	2212	71.2	915	5	ABG95166	Human GPC
44	2210	71.1	915	2	ABR80479	Rat metab
45	2210	71.1	915	6	AAE30199	Rat metab

ALIGNMENTS

RESULT 1

ABR56244
ID ABR56244 standard; protein; 584 AA.

AC ABR56244;

DT 20-NOV-2003 (first entry)

DE Rat glutamic acid receptor.

KW Rat; anorectic; antiulcer; antidiabetic; laxative; antidiarrheic;

glutamic acid receptor; receptor; gastrointestinal tract disorder;
sitiefirgia; obesity; ulcer; diabetes; constipation; diarrhoea.

OS Rattus norvegicus.

PN WO2003035873-A1.

PD 01-MAY-2003.

PF 23-OCT-2002; 2002WO-JP010984.

PR 23-OCT-2001; 2001JP-00325159.

PA (AJIN) AJINOMOTO CO INC.

PI San Gabriel A, Maekawa T, Uneyama H, Torii K;

DR WPI; 2003-430418/40.

DR N-PSDB; ACC70676.

Novel glutamic acid receptor protein and encoded DNA, applicable in screening agonists or antagonists of glutamic acid or allosteric modulator for use as drugs in ameliorating symptoms and diseases e.g. obesity.

Claim 3; Page 33-35; 39pp; Japanese.

The present sequence is the protein sequence for rat glutamic acid receptor. The receptor has a transmembrane domain and an intracellular domain common to type 4 metabotropic glutamic acid receptor protein, and an extracellular domain shorter by 316 or 327 amino acid residues than type 4 metabotropic glutamic acid receptor protein. The receptor and its coding sequence are useful in screening agonists or antagonists of glutamic acid or allosteric modulator for use as drugs in ameliorating symptoms and diseases due to abnormal metabolism in gastrointestinal tract including small and large intestines e.g. sitiefirgia, obesity, ulcer, diabetes, constipation and diarrhoea.

```

XX SQ Sequence 584 AA;
Query Match 100.0%; Score 3107; DB 6; Length 584;
Best Local Similarity 100.0%; Pred. No. 6.4e-314;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPGVSSSLPTMTSGDFRYSFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKC 60
Db 1 MPGVSSSLPTMTSGDFRYSFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKC 60

Qy 61 TNRRIGQDSAYEQEGKQVFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 120
Db 61 TNRRIGQDSAYEQEGKQVFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 120

Qy 121 YIRNVNFSGIAGNPVTNFNGDAPGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERMQW 180
Db 121 YIRNVNFSGIAGNPVTNFNGDAPGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERMQW 180

Qy 181 PGGQQLPRSSICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240
Db 181 PGGQQLPRSSICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPT 240

Qy 241 NRTSQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRELSYV 300
Db 241 NRTSQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRELSYV 300

Qy 301 LLAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSV 360
Db 301 LLAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSV 360

Qy 361 SAPRISPASOLATFILLISQLLIGICVWFVVDPSHVSVDQDORTLDPFARGVLKCDI 420
Db 361 SAPRISPASOLATFILLISQLLIGICVWFVVDPSHVSVDQDORTLDPFARGVLKCDI 420

Qy 421 SDLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFGT 480
Db 421 SDLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFGT 480

Qy 481 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAAT 540
Db 481 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAAT 540

Qy 541 MSNFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584
Db 541 MSNFTQGNFRPNGEAKSELCELENLETPALATKQTYVYTNHAI 584

RESULT 2
ABG74133
ID ABG74133 standard; protein; 604 AA.
XX
AC ABG74133;
XX
DT 03-APR-2003 (first entry)
XX
DE Rat metabotropic glutamate receptor mGluR4.
XX
KW Rat; metabotropic glutamate receptor; mGluR4; umami; taste; receptor;
KW umami mimicking compound; monosodium L-glutamate; CAMP.
XX
OS Rattus sp.
XX
FN US2002151052-A1.
XX
PD 17-OCT-2002.
XX
PF 30-MAR-2001; 2001US-00820809.
XX
PR 31-MAR-2000; 2000US-0193454P.
XX
PA (UYMI-) UNIV MIAMI.
XX

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PI Chaudhari N, Roper SD;
XX WPI: 2003-182515/18.
DR N-PSDB; ABX16077.
XX
PT Novel metabotropic glutamate taste receptor which functions as a umami
PT taste receptor, useful for screening for umami mimicking compounds.
XX
PS Claim 1; Page 7; 23pp; English.
XX
CC The invention relates to a rat metabotropic glutamate taste receptor
CC having a molecular weight of 68 kDa, mGluR4, appearing as ABG74133. Also
CC included are an isolated mRNA molecule encoding mGluR4 appearing as
CC ABX16077 (rat sequence) and the human homologue appearing as ABX16087, a
CC mammalian cell transfected with cDNA encoding mGluR4 (the cDNA expressed
CC in the mammalian cell is capable of being translated into immunologically
CC recognisable metabotropic glutamate taste receptors) and screening
CC samples for umami mimicking compounds (comprising: (a) transfecting
CC mammalian cells with an isolated rat cDNA encoding metabotropic glutamate
CC taste receptor; (b) culturing the transfected cells in an environment
CC that promotes expression of immunologically recognisable metabotropic
CC glutamate taste receptors; (c) treating the transfected cells with a
CC compound that induces CAMP production; (d) incubating the cells with a
CC sample containing a potential umami mimicking compound capable of binding
CC to the metabotropic glutamate taste receptors; (e) measuring the amount
CC of CAMP produced; and (f) correlating suppression of CAMP production with
CC umami mimicking compound binding to the metabotropic glutamate taste
CC receptors). The mGluR4 functions as a umami taste receptor, and responds
CC to monosodium L-glutamate binding by decreasing cellular level of CAMP.
CC The cell is useful for screening samples for umami mimicking compounds.
CC The mGluR4 is useful for screening for umami mimics. The present sequence
CC represents the rat mGluR4 protein
XX
SQ Sequence 604 AA;

```

```

Query Match 98.2%; Score 3050.5; DB 6; Length 604;
Best Local Similarity 98.6%; Pred. No. 5.2e-308;
Matches 575; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 3 GVSSSLPTMT-SGDFRYSFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 22 GAVTILPKRMSVGRGDFRYSFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKGSHIKKCT 81

Qy 62 NRERIGQDSAYEQEGKQVFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 121
Db 82 NRERIGQDSAYEQEGKQVFVIDAVYANGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLK 141

Qy 122 IRNVNFSGIAGNPVTNFNGDAPGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERMQWP 181
Db 142 IRNVNFSGIAGNPVTNFNGDAPGRYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERMQWP 201

Qy 182 GSGQQLPRSSICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 241
Db 202 GSGQQLPRSSICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 261

Qy 242 RTSQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRELSYVL 301
Db 262 RTSQPIPIVKLEWDSWAVLPLFLAVVGIAATLFVVVTFVRYNDTPIVKASGRELSYVL 321

Qy 302 LAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSVS 361
Db 322 LAGIFLCYATTFMLIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSVS 381

Qy 362 APRFISPASOLATFILLISQLLIGICVWFVVDPSHVSVDQDORTLDPFARGVLKCDIS 421
Db 382 APRFISPASOLATFILLISQLLIGICVWFVVDPSHVSVDQDORTLDPFARGVLKCDIS 441

Qy 422 DLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFGTS 481
Db 442 DLSLICLLGYSMLLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPFGTS 501

Qy 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAATM 541
Db 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAATM 541

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Db 502 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQNVPKKSLKAVVTAATM 561

QY 542 SNKFTQGNFRPNNGEAKSELNLETPALATKQTVVYTNHAI 584

Db 562 SNKFTQGNFRPNNGEAKSELNLETPALATKQTVVYTNHAI 604

RESULT 3

AD58164

ID ADE58164 standard; protein; 912 AA.

AC ADE58164;

XX 29-JAN-2004 (first entry)

DT Rat Protein P31423, SEQ ID NO 4035.

DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

OS WO2003016475-A2.

PN 27-FEB-2003.

PD 14-AUG-2002; 2002WO-US025765.

PF 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'ureo D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P31423.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 912 AA;

Query Match 98.2%; Score 3050.5; DB 7; Length 912;

Best Local Similarity 98.6%; Pred. No. 9.7e-308;

Matches 575; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 3 GVSSSLPTMT-SGDRYFSSRTLNNRRNTWFAEFWEDNFHCKLSRHAKKGSHIKKCT 61

Db 330 GAVTILPKRMSVRGPDYFSSRTLNNRRNTWFAEFWEDNFHCKLSRHAKKGSHIKKCT 389

QY 62 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMHRDLCPCRGVGLCPRMDPVDGTQLLKY 121

Db 390 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMHRDLCPCRGVGLCPRMDPVDGTQLLKY 449

QY 122 IRNVNFSGIAGNPVTFNENGDAPEGRIYQVQLRNGSAEYKVGISWTDLHLRIERMOWP 181

Db 450 IRNVNFSGIAGNPVTFNENGDAPEGRIYQVQLRNGSAEYKVGISWTDLHLRIERMOWP 509

QY 182 GSGQQLPRSI CSLPCQGERKKTVMGACCHCEPCTGYOVQVDRYTKCTCPYDMRPTEN 241

Db 510 GSGQQLPRSI CSLPCQGERKKTVMGACCHCEPCTGYOVQVDRYTKCTCPYDMRPTEN 569

QY 242 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIATLFWVVTFRYNDTPIVKASGRELSYVL 301

Db 570 RTSCQPIPIVKLEWDSWAVLPLFLAVVGIATLFWVVTFRYNDTPIVKASGRELSYVL 629

QY 302 LAGIFLCYATTFLMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361

Db 630 LAGIFLCYATTFLMTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 689

QY 362 APRFISPASQLAITFILISLQLLGCVMFVVDPSHSVDFQDORTLDRPFARGVLKCDIS 421

Db 690 APRFISPASQLAITFILISLQLLGCVMFVVDPSHSVDFQDORTLDRPFARGVLKCDIS 749

QY 422 DLSLILCLLGYSMLLMVTCTVYAIKTRGVPETFPNEAKPIGFTMYTTCIVMLAFIPFPFGTS 481

Db 750 DLSLILCLLGYSMLLMVTCTVYAIKTRGVPETFPNEAKPIGFTMYTTCIVMLAFIPFPFGTS 809

QY 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQNVPKKSLKAVVTAATM 541

Db 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQNVPKKSLKAVVTAATM 869

QY 542 SNKFTQGNFRPNNGEAKSELNLETPALATKQTVVYTNHAI 584

Db 870 SNKFTQGNFRPNNGEAKSELNLETPALATKQTVVYTNHAI 912

RESULT 4

AD58168

ID ADE58168 standard; protein; 912 AA.

XX ADE58168;

AC ADE58168;

DT 29-JAN-2004 (first entry)

XX Rat Protein P31423, SEQ ID NO 4039.

DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

OS WO2003016475-A2.

PN 27-FEB-2003.

PD 14-AUG-2002; 2002WO-US025765.

PF 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

PA

CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 909 AA;

Query Match 97.1%; Score 3017; DB 8; Length 909;
 Best Local Similarity 97.8%; Pred. No. 3e-304;
 Matches 570; Conservative 3; Mismatches 8; Indels 2; Gaps 2;
 QY 3 GVSSSLPTMT-SGDRYFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 61
 DB 328 GAVTILPKRTSRGDFRYSFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 387
 QY 62 NREIGQDSAYEKGKQVFIDAVYAMGHALHAMHDLCPGRVGLCPRMDPDVGTQLLKY 121
 DB 388 NREIGQDSAYEKGKQVFIDAVYAMGHALHAMHDLCPGRVGLCPRMDPDVGTQLLKY 447
 QY 122 IRNVNFSGIAGNPVTNENGDPAGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMOWP 181
 DB 448 IRNVNFSGIAGNPVTNENGDPAGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMOWP 507
 QY 182 GSGQQLPRISICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 241
 DB 508 GSG-QLPRISICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 566
 QY 242 RTSCQPIPIVKLEWDSWPAVLPLFLAVVGIAATLFVVTFFRYNDTPIVKASGRELSTYL 301
 DB 567 RTSCQPIPIVKLEWDSWPAVLPLFLAVVGIAATLFVVTFFRYNDTPIVKASGRELSTYL 626
 QY 302 LAGIFLCYATTFILMIAEPDLGTCSLRRIIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361
 DB 627 LAGIFLCYATTFILMIAEPDLGTCSLRRIIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 686
 QY 362 APRFISPASQLAITFILISLQLGICVWFVDPSPSHVDFQDQRTLDPRFARGVLKCDIS 421
 DB 687 APRFISPASQLAITFILISLQLGICVWFVDPSPSHVDFQDQRTLDPRFARGVLKCDIS 746
 QY 422 DLSLICLLGYSMLLMTCTVYAIKTRGVPTNEAKPIGFTWYTCIVMLAIPFPGTS 481
 DB 747 DLSLICLLGYSMLLMTCTVYAIKTRGVPTNEAKPIGFTWYTCIVMLAIPFPGTS 806
 QY 482 QSADKLYIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKESLKAIVTAATM 541
 DB 807 QSADKLYIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKESLKAIVTAATM 866
 QY 542 SNKFTQGNFRPNGEAKSELNLETPALATKQTYVYTNHAI 584
 DB 867 SNKFTQGNFRPNGEAKSELNLETPALATKQTYVYTNHAI 909

RESULT 6

AA015101
 ID AA015101 standard; protein; 909 AA.
 XX AA015101;
 AC
 DT 29-AUG-2003 (revised)
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ph8SPmGluR4 chimeric protein.
 DE Human; G-protein fusion receptor; extracellular domain;
 KW transmembrane domain; intracellular domain; Car; mGluR; GABABR;
 KW modulator identification.
 XX
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO200229033-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US031074.
 XX
 PR 03-OCT-2000; 2000US-00679664.
 XX
 PA (NPSF-) NPS PHARM INC.
 XX
 PI Storrman T, Hammerland LG, Storjohann LL, Busby JG, Garrett JB;
 PI Simin RT;
 XX
 DR WPI; 2002-330170/36.
 XX
 PT Novel G-protein fusion receptor, useful for identifying modulators of
 PT Car, mGluR and GABABR, comprises G-protein joined to the intracellular
 PT domain of the receptor.
 XX
 PS Disclosure; Fig 16; 168pp; English.
 CC
 CC The invention comprises G-protein fusion receptors - comprising
 CC extracellular, transmembrane and intracellular domains similar to Car,
 CC mGluR or GABAB receptor sequences. The G-protein fusion receptors of the
 CC invention may also possess a linker joined to the carboxy terminus of the
 CC intracellular domain, and a G-protein joined to the linker. The G-protein
 CC fusion receptors of the invention are useful for identifying modulators
 CC of Car, mGluR and GABABR for use in treating associated conditions. The
 CC present amino acid sequence was used in the production of the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 909 AA;
 Query Match 96.7%; Score 3004.5; DB 5; Length 909;
 Best Local Similarity 96.7%; Pred. No. 6e-303;
 Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
 QY 3 GVSSSLPTMT-SGDRYFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 61
 DB 327 GAVTILPKRMSVRGDFRYSFSSRTLDNNRNINFAEFWEDNFHCKLSRHALKGSHIKKCT 386
 QY 62 NREIGQDSAYEKGKQVFIDAVYAMGHALHAMHDLCPGRVGLCPRMDPDVGTQLLKY 121
 DB 387 NREIGQDSAYEKGKQVFIDAVYAMGHALHAMHDLCPGRVGLCPRMDPDVGTQLLKY 446
 QY 122 IRNVNFSGIAGNPVTNENGDPAGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMOWP 181
 DB 447 IRNVNFSGIAGNPVTNENGDPAGRYDIYQQLRNGSAEYKVGISWTDLHLRIERMOWP 506
 QY 182 GSGQQLPRISICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 241
 DB 507 GSGQQLPRISICSLPCQGERKKTVMGACCHCEPCTGYQYQVDRYTKCTCPYDMRPTEN 566
 QY 242 RTSCQPIPIVKLEWDSWPAVLPLFLAVVGIAATLFVVTFFRYNDTPIVKASGRELSTYL 301
 DB 567 RTGCRPIPIIKLEWGSWPAVLPLFLAVVGIAATLFVVTFFRYNDTPIVKASGRELSTYL 626

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QY 302 LAGIFLCYATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 627 LAGIFLCYATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 686
QY 362 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 421
Db 687 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 746
QY 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNEAKPIGFTMYTTCIVWLAFIPFPGTS 481
Db 747 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNEAKPIGFTMYTTCIVWLAFIPFPGTS 806
QY 482 QSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPQONVPKRKSLKAVVTAATM 541
Db 807 QSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPQONVPKRKSLKAVVTAATM 866
QY 542 SNKFTQGNFRPNGBAKSELCELENLETPALATKQTYVTYTNHAI 584
Db 867 SNKFTQGNFRPNGBAKSELCELENLEAPALATKQTYVTYTNHAI 909

RESULT 7
AAR82658
ID AAR82658 standard; protein; 912 AA.
AC AAR82658;
XX
XX
XX 20-DEC-1995 (first entry)
XX Human mGluR4.
XX Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;
KW Alzheimer disease; detection; diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 588..610
FT /label= TMD-I
FT /note= "transmembrane domain I"
FT 625..645
FT /label= TMD-II
FT /note= "transmembrane domain II"
FT 657..675
FT /label= TMD-III
FT /note= "transmembrane domain III"
FT 699..720
FT /label= TMD-IV
FT /note= "transmembrane domain IV"
FT 751..771
FT /label= TMD-V
FT /note= "transmembrane domain V"
FT 786..807
FT /label= TMD-VI
FT /note= "transmembrane domain VI"
FT 823..847
FT /label= TMD-VII
FT /note= "transmembrane domain VII"
XX
XX W09522609-A2.
XX
XX 24-AUG-1995.
XX
XX 21-FEB-1995; 95WO-GB0000356.
XX
XX 21-FEB-1994; 94GB-00003285.
XX
XX 01-AUG-1994; 94GB-00015532.
XX
XX (WELL ) WELLCOME FOUND LTD.
XX
XX Makoff AJ;
XX

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DR WPI; 1995-302715/39.
DR N-PSDB; AAT03888.
XX
XX New isolated human metabotropic glutamate receptors - used for detection,
XX diagnosis and therapy of diseases associated with the receptors, eg.
XX stroke, epilepsy and Alzheimer's disease.
XX
XX Claim 2; Page 40-43; 55pp; English.
XX
XX mRNA from the human cerebellum was used to construct a cDNA library. cDNA
XX was amplified by PCR primers (AAT03896-97) based on rat mGluR4 sequences
XX and with the primers given in AAT03898-99 to obtain cDNA encoding human
XX mGluR4
XX
XX Sequence 912 AA;
XX
XX Query Match 96.7%; Score 3004.5; DB 2; Length 912;
XX Best Local Similarity 96.7%; Pred. No. 6e-303;
XX Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
QY 3 GVSSSLPRTMT-SGFDRYFSSRTLDDNNRNINWFAEFWEDNFHCKLSRHALKKGSHIKKCT 61
Db 330 GAVTILPKRMSVGFDRYFSSRTLDDNNRNINWFAEFWEDNFHCKLSRHALKKGSHVKKCT 389
QY 62 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLKY 121
Db 390 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAMHRDLCPGRVGLCPRMDPVDGTQLLKY 449
QY 122 IRNVNFSGIAGNPVTNENGDAPEGRIYDIYQQLRNGSAEYKVIGSWTDHLHLRIERMQWP 181
Db 450 IRNVNFSGIAGNPVTNENGDAPEGRIYDIYQQLRNGSAEYKVIGSWTDHLHLRIERMHP 509
QY 182 GSGQQLPRSCSLPCQGBERKTKVKGACWHCEPCTGYQYQVDRYTKCTCPYDMRPTE 241
Db 510 GSGQQLPRSCSLPCQGBERKTKVKGMPCCWHCEPCTGYQYQVDRYTKCTCPYDMRPTE 569
QY 242 RTSCQPIPIVLEWDSWAVLPLFLAVVGIAATLFFVVVTFVRYNDTPIVKASGRELSYVL 301
Db 570 RTGCRPIPIKLEWGSWAVLPLFLAVVGIAATLFFVITFVRYNDTPIVKASGRELSYVL 629
QY 302 LAGIFLCYATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
Db 630 LAGIFLCYATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689
QY 362 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 421
Db 690 APRFISPASQLAITFILISLQLLGICVWFVVDPSHVSVDFOQRTLDPRFARGVLKCDIS 749
QY 422 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNEAKPIGFTMYTTCIVWLAFIPFPGTS 481
Db 750 DLSLICLLGYSMMLMVTCTVVAIKTRGVPETFNEAKPIGFTMYTTCIVWLAFIPFPGTS 809
QY 482 QSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPQONVPKRKSLKAVVTAATM 541
Db 810 QSADKLYIQTTTLTVSVSLSASVSLGMLYMPKVYIILFHPQONVPKRKSLKAVVTAATM 869
QY 542 SNKFTQGNFRPNGBAKSELCELENLETPALATKQTYVTYTNHAI 584
Db 870 SNKFTQGNFRPNGBAKSELCELENLEAPALATKQTYVTYTNHAI 912

RESULT 8
AAR23757
ID AAR23757 standard; protein; 912 AA.
XX
XX AAR23757;
XX AC
XX 10-SEP-2002 (first entry)
XX
XX Human metabotropic glutamate (mGluR4) receptor protein.
XX
XX Human; metabotropic glutamate receptor; mGluR4; neurodegeneration;
XX antipsychotic; anticonvulsant; analgesic; antidepressant; antiemetic.
XX

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XX Homo sapiens.
 XX US6384205-B1.
 XX 07-MAY-2002.
 XX 18-AUG-2000; 2000US-00641318.
 XX 12-MAR-1996; 96US-0013189P.
 XX 12-MAR-1997; 97US-00816178.
 XX (ELIL) LILLY & CO ELI.
 XX Belagaje RM, Wu S;
 XX WPI; 2002-442818/47.
 XX N-PSDB; AAD38024, AAD38025.
 XX New nucleic acid encoding human metabotropic glutamate receptor, useful
 PT e.g. in screening for specific agonists and antagonists for treating e.g.
 PT neurodegeneration.
 XX Claim 1; Col 9-16; 35pp; English.
 XX The present invention relates to human metabotropic glutamate receptor
 CC (mGluR4) proteins and polynucleotides encoding such proteins. mGluR4
 CC sequences of the invention are useful for treating acute and chronic
 CC neurodegeneration. They are also used as antipsychotic, anticonvulsant,
 CC analgesic, antidepressant and anxiolytic agents. They are also useful for
 CC the diagnosis and/or treatment of conditions associated with an excess or
 CC deficiency of mGluR4. The present sequence is human mGluR4 protein
 XX Sequence 912 AA;
 SQ

Query Match 96.7%; Score 3004.5; DB 5; Length 912;
 Best Local Similarity 96.7%; Pred. No. 68-303;
 Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
 3 GVSSSLPTMT-SGDRYFSSRTLDNRRNIWFAFWEDNPFCKLSRHAKKGSHKCT 61
 330 GAVTILPKMSVGRGDFYSSRTLDNRRNIWFAFWEDNPFCKLSRHAKKGSHKCT 389
 62 NREIGQDSAYQEGKVQVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 121
 390 NREIGQDSAYQEGKVQVIDAVYAMGHAMHARDLCPGRVGLCPRMDPVDGTQLKY 449
 122 IRNVFSGIAGNPVTFNENGDPGRYDIYQYLRNDSAEYKVGISWTDHLHLRIERMHP 181
 450 IRNVFSGIAGNPVTFNENGDPGRYDIYQYLRNDSAEYKVGISWTDHLHLRIERMHP 509
 182 GSGQQLPRISICSLPCQGERKKTVMGACCWCEPCTGYQYQVDRYTKTCYDMRPTEN 241
 510 GSGQQLPRISICSLPCQGERKKTVMGACCWCEPCTGYQYQVDRYTKTCYDMRPTEN 569
 242 RTSCQPIPIKLEWSPWAVLFLAVGVIAATLFWVTFVRYNDTPIVKASGRELSYVL 301
 570 RTGCRPIPIKLEWSPWAVLFLAVGVIAATLFWVTFVRYNDTPIVKASGRELSYVL 629
 302 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALTNTNRIYRIFEQGRSVS 361
 630 LAGIFLCVATTFMLTAEPDLGTCSLRRIFLGLGMSISYAALTNTNRIYRIFEQGRSVS 689
 362 APRFTSPASQALAITFLISLQLGICWFPVDPSPHVDVDFQDRLDFRARGVLKCDIS 421
 690 APRFTSPASQALAITFLISLQLGICWFPVDPSPHVDVDFQDRLDFRARGVLKCDIS 749
 422 DLISLCLLGYSMLLWTCVYAIKTRGVPETNEAKPIGFTMYTTCIVWLAFIPFFGTS 481
 750 DLISLCLLGYSMLLWTCVYAIKTRGVPETNEAKPIGFTMYTTCIVWLAFIPFFGTS 809
 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAATM 541

Db 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAATM 869
 QY 542 SNKFTQKGNFRPNGEAKSELCELTALATKQTIVTYTNHAI 584
 Db 870 SNKFTQKGNFRPNGEAKSELCELTALATKQTIVTYTNHAI 912
 RESULT 9
 ABP81846
 ID ABP81846 standard, protein; 912 AA.
 XX AC ABP81846;
 XX DT 04-MAR-2003 (first entry)
 XX DE Human metabotropic glutamate receptor 4 protein SEQ ID NO:176.
 XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 XX ulcer.
 XX OS Homo sapiens.
 XX PN WO200261087-A2.
 XX PD 08-AUG-2002.
 XX PF 19-DEC-2001; 2001WO-US050107.
 XX PR 19-DEC-2000; 2000US-0257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX PI Burner GC, Roush CL, Brown JP;
 XX WPI; 2003-046718/04.
 XX N-PSDB; ABZ42692.
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX Disclosure; Fig 1; 523pp; English.
 XX The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 912 AA;

Query Match 96.7%; Score 3004.5; DB 6; Length 912;
Best Local Similarity 96.7%; Pred. No. 6e-303;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
Qy 3 GVSSSLPRMT-SGFDYFSSRTLNNRRNIWFAEFWEDNFCKLSRHALLKGGSHIKCT 61
Db 330 GAVTILPKRMSVGRGDFYFSSRTLNNRRNIWFAEFWEDNFCKLSRHALLKGGSHVKKCT 389
Qy 62 NRERIGQDSAYEQEGKQVFVIDAVYAMGHALHAMHRDLCPRGVLGCPRMDPVDGTQLLKY 121
Db 390 NRERIGQDSAYEQEGKQVFVIDAVYAMGHALHAMHRDLCPRGVLGCPRMDPVDGTQLLKY 449
Qy 122 IRNVNFGSIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKIVGSSWTDLHLRIERMOWP 181
Db 450 IRNVNFGSIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKIVGSSWTDLHLRIERMOWP 509
Qy 182 GSGQQLPRISICSLPCQPGERKKTVMKGMCCWHCEPCTGYQVQVDRYTKCTCPYDMRPTE 241
Db 510 GSGQQLPRISICSLPCQPGERKKTVMKGMCCWHCEPCTGYQVQVDRYTKCTCPYDMRPTE 569
Qy 242 RTSQOPIPIVKLEWDSWAVLPLFLAVVGIAATLFLVYVYVYVYVYVYVYVYVYVYVYVY 301
Db 570 RTGCRPIPIIKLEWGSWAVLPLFLAVVGIAATLFLVYVYVYVYVYVYVYVYVYVYVYVY 629
Qy 302 LAGIFLCVATTLMTAEPLDGLTSLRRPLGLGMSISYAALLTKTNRIYRIFEQGKRSVS 361
Db 630 LAGIFLCVATTLMTAEPLDGLTSLRRPLGLGMSISYAALLTKTNRIYRIFEQGKRSVS 689
Qy 362 APRFISPASQALITFILISLQLLGICVWFVDPSPHSVDFDQRTLDPRFARGVLKCDIS 421
Db 690 APRFISPASQALITFILISLQLLGICVWFVDPSPHSVDFDQRTLDPRFARGVLKCDIS 749
Qy 422 DLSLCLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPIFFGTS 481
Db 750 DLSLCLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVWLAFIPIFFGTS 809
Qy 482 QSADKLYIQTTLTVSVLSASVSLGMLYKPVYIILFHPQONVPRKRSILKAVVTAATM 541
Db 810 QSADKLYIQTTLTVSVLSASVSLGMLYKPVYIILFHPQONVPRKRSILKAVVTAATM 869
Qy 542 SNKFTQKGNFRNGEAKSELNLETPALATKQTVYVYVYVYVYVYVYVYVYVYVYVYVY 584
Db 870 SNKFTQKGNFRNGEAKSELNLETPALATKQTVYVYVYVYVYVYVYVYVYVYVYVYVY 912

RESULT 10
ADE58170
ID ADE58170 standard; protein; 912 AA.
XX
AC ADE58170;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q14833, SEQ ID NO 4041.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
XX
PT GENBANK; Q14833.
PT
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS
XX
CC Claim 1; Page; 1017pp; English.
CC
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 912 AA;

Query Match 96.7%; Score 3004.5; DB 7; Length 912;
Best Local Similarity 96.7%; Pred. No. 6e-303;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
Qy 3 GVSSSLPRMT-SGFDYFSSRTLNNRRNIWFAEFWEDNFCKLSRHALLKGGSHIKCT 61
Db 330 GAVTILPKRMSVGRGDFYFSSRTLNNRRNIWFAEFWEDNFCKLSRHALLKGGSHVKKCT 389
Qy 62 NRERIGQDSAYEQEGKQVFVIDAVYAMGHALHAMHRDLCPRGVLGCPRMDPVDGTQLLKY 121
Db 390 NRERIGQDSAYEQEGKQVFVIDAVYAMGHALHAMHRDLCPRGVLGCPRMDPVDGTQLLKY 449
Qy 122 IRNVNFGSIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKIVGSSWTDLHLRIERMOWP 181
Db 450 IRNVNFGSIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYKIVGSSWTDLHLRIERMOWP 509
Qy 182 GSGQQLPRISICSLPCQPGERKKTVMKGMCCWHCEPCTGYQVQVDRYTKCTCPYDMRPTE 241
Db 510 GSGQQLPRISICSLPCQPGERKKTVMKGMCCWHCEPCTGYQVQVDRYTKCTCPYDMRPTE 569
Qy 242 RTSQOPIPIVKLEWDSWAVLPLFLAVVGIAATLFLVYVYVYVYVYVYVYVYVYVYVYVY 301
Db 570 RTGCRPIPIIKLEWGSWAVLPLFLAVVGIAATLFLVYVYVYVYVYVYVYVYVYVYVYVY 629

QY 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361
 DB 630 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 689
 QY 362 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDVDFDQDRTLDPRFARGVLKCDIS 421
 DB 690 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDVDFDQDRTLDPRFARGVLKCDIS 749
 QY 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 481
 DB 750 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 809
 QY 482 QSAKDLXIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKRSKLVAVTAATM 541
 DB 810 QSAKDLXIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKRSKLVAVTAATM 869
 QY 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYTNHAI 584
 DB 870 SNKFTQGNFRPNGEAKSELCELENLEAPALATKQTVVYTNHAI 912

RESULT 11

AD58166
 ID ADE58166 standard; protein; 912 AA.

XX AC ADE58166;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein Q14833, SEQ ID NO 4037.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW spated nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX XX (GHEO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Belfort K, Costigan M;

XX DR WPI: 2003-268312/26.

XX DR GENBANK; Q14833.

XX PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 912 AA;

Query Match 96.7%; Score 3004.5; DB 7; Length 912;

Best Local Similarity 96.7%; Pred. No. 6e-303;

Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 3 GVSSSLPTRMT-SGPDYRFSSRTLNNRRNINWFAEFWEDNPHCKLSRHALKGSHIKKCT 61

DB 330 GAVTILPKRMSVGRGDRYFSSRTLNNRRNINWFAEFWEDNPHCKLSRHALKGSHVKKCT 389

QY 62 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHMRDLCPRGVGLCPRMDPVDGTQLLKY 121

DB 390 NRERIGQDSAYEQEGKVQFVIDAVYAMGHALHMRDLCPRGVGLCPRMDPVDGTQLLKY 449

QY 122 IRNVNFSGIAGNPVTENGDAPGRYDIYQVLRNGSAEYKVGISWTDLHLRIERMQWP 181

DB 450 IRNVNFSGIAGNPVTENGDAPGRYDIYQVLRNGSAEYKVGISWTDLHLRIERMHWP 509

QY 182 GSGQQLPRISICSLPCQGERKKTVKGMACCWHCEPCTGYQVODRYTCTCYDNRPTEN 241

DB 510 GSGQQLPRISICSLPCQGERKKTVKGMCCWHCEPCTGYQVODRYTCTCYDNRPTEN 569

QY 242 RTSQPIPIVKLEWDSWAVLPLFLAVVGVIAATLFVVVTVFVRYNDTPIVKASGRELSTYL 301

DB 570 RTGCRPIPIKLEWGSWAVLPLFLAVVGVIAATLFVVVTVFVRYNDTPIVKASGRELSTYL 629

QY 302 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 361

DB 630 LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIPEQGRSVS 689

QY 362 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDVDFDQDRTLDPRFARGVLKCDIS 421

DB 690 APRFISPASQALAITFILISLQLLIGICVWFVDPSSHVDVDFDQDRTLDPRFARGVLKCDIS 749

QY 422 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 481

DB 750 DLSLICLLGYSMMLMVTCTVYAIKTRGVPTFNEAKPIGFTMYTTCIVMLAPIPIFFGTS 809

QY 482 QSAKDLXIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKRSKLVAVTAATM 541

DB 810 QSAKDLXIQTTLTIVSVLSASVSLGMLYMPKYIILFHPQONVPRKRSKLVAVTAATM 869

QY 542 SNKFTQGNFRPNGEAKSELCELENLETPALATKQTVVYTNHAI 584

DB 870 SNKFTQGNFRPNGEAKSELCELENLEAPALATKQTVVYTNHAI 912

RESULT 12

AD029094

ID AD029094 standard; protein; 912 AA.

XX AC AD029094;

XX DT 29-JUL-2004 (first entry)

XX DE Human novel GPCR GRM4, SEQ ID NO:193.

XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;

KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianaemic; antieborrheic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
XX Homo sapiens.
XX
XX WO2004040000-A2.
XX
XX 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.
XX
XX 09-SEP-2003; 2002US-0409303P.
XX
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
XX
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
XX WPI: 2004-390329/36.
XX
XX N-PSDB; AD029776.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX
XX Claim 1; SEQ ID NO 193; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene of the invention; a mouse comprising a
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
XX invention further discloses variants of the GPCR polypeptides and vectors
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
XX be used in the diagnosis, treatment or prevention of a wide variety of
XX diseases including neurological disorders (e.g., Alzheimer's disease,
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
XX disorders of the adrenal gland; disorders of the colon or intestine
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
XX myocardial infarction); muscular disorders; blood disorders (e.g.,
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
XX thyroid (e.g., cancers). The present sequence represents a GPCR of the
XX invention. Note: The full sequence data for this patent did not form part
XX of the printed specification; those sequences not shown were obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

3Q Sequence 912 AA;
Query Match 96.7%; Score 3004.5; DB 8; Length 912;
Best Local Similarity 96.7%; Pred. No. 6e-303;
Matches 564; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
QY 3 GVSSSLPRMT-SGDFRYFSRSLDNNRRNIWFAEFWEDNFHCKLSRHALKKSGSHKCT 61
DB 330 GAVTILPKRMSVGRFDYFSSRTLDNNRRNIWFAEFWEDNFHCKLSRHALKKSGSHKCT 389
QY 62 NRERIGDSAYEQSGKVQFVIDAVYAMGHAMHMRDLCPGRVGLCPRMDPVDGTQLLY 121
DB 390 NRERIGDSAYEQSGKVQFVIDAVYAMGHAMHMRDLCPGRVGLCPRMDPVDGTQLLY 449
QY 122 IRNVNFSGIAGNPVTNENGDAFGYDIYQYQLENGSAEYKVIQSWTDHLHLRLRHWCP 181
DB 450 IRNVNFSGIAGNPVTNENGDAFGYDIYQYQLENGSAEYKVIQSWTDHLHLRLRHWCP 509
QY 182 GSGQQLPRISCSLPCQPGERKKTVMKMACCWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 241
DB 510 GSGQQLPRISCSLPCQPGERKKTVMKMACCWHCEPCTGYQYQVDRYCTCTCPYDMRPTEN 569
QY 242 RTSCQPIPIVLEWDSWPAVLPLFLAVVGTAAATLFFVVVTFVRYNDTPIVKAAGRELSYVL 301
DB 570 RTGCRPIPIIKLEWGSWPAVLPLFLAVVGTAAATLFFVVVTFVRYNDTPIVKAAGRELSYVL 629
QY 302 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 361
DB 630 LAGIFLCVATTFELMIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRSVS 689
QY 362 APREISPASQLAITFLLISLQLLGICVFWVVDPSHVVDFQDQRTLDPRFARGVLCDDIS 421
DB 690 APREISPASQLAITFLLISLQLLGICVFWVVDPSHVVDFQDQRTLDPRFARGVLCDDIS 749
QY 422 DLSLICLLGYSMILLMTCTVVAIKTRGVPEFNEAKDPIGFTMYTTCIVWLAFIPFGTS 481
DB 750 DLSLICLLGYSMILLMTCTVVAIKTRGVPEFNEAKDPIGFTMYTTCIVWLAFIPFGTS 809
QY 482 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVIIILFHPQONVPEKRSLSKAVVTAATM 541
DB 810 QSADKLYIQTTLTVSVLSASVSLGMLYMPKVIIILFHPQONVPEKRSLSKAVVTAATM 869
QY 542 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTVYTNHAI 584
DB 870 SNKFTQKGNFRPNGEAKSELCELENLETPALATKQTYVTVYTNHAI 912
RESULT 13
ADQ89114
ID ADQ89114 standard; protein; 912 AA.
XX
AC ADQ89114;
XX
XX 21-OCT-2004 (first entry)
DT
XX
DE Human urological disorder related protein 115 SEQ:66.
XX
XX urological disorder; uropathic; cytostatic; urinary incontinence;
KW benign prostatic hyperplasia; human.
XX
OS Homo sapiens.
XX
XX WO2004065576-A2.
XX
XX 05-AUG-2004.
XX
XX 14-JAN-2004; 2004WO-US0000750.
XX
XX 15-JAN-2003; 2003US-0440318P.
XX
XX 04-FEB-2003; 2003US-0444783P.
XX
XX 27-MAR-2003; 2003US-0457901P.
XX
XX 08-MAY-2003; 2003US-0468775P.
XX
XX 19-MAY-2003; 2003US-0471614P.

QY	182	GSGQQLPRSICSLPCQPGERKKTVKGMACCWHCEBCTGYQYQVDRYTCKTCPDMEPTEN	241
DB	510	GSGQQLPRSICSLPCQPGERKKTVKGMPCCWHCEBCTGYQYQVDRYTCKTCPDMEPTEN	569
QY	242	RTSQCPIPIVKLEWSPNAVLPLFLAVVGIIAATLFFVVTVFVRNDTPIVKASGRELSYVL	301
DB	570	RTGCRPIPIKLEWSPNAVLPLFLAVVGIIAATLFWITVFVRNDTPIVKASGRELSYVL	629
QY	302	LAGIFLCYATTFLMTAEAPDLGTCSLRRRIFLGIGHMSISYAALLTKTNRIYRIFEQGKRYSVS	361
DB	630	LAGIFLCYATTFLMTAEAPDLGTCSLRRRIFLGIGHMSISYAALLTKTNRIYRIFEQGKRYSVS	689
QY	362	APRFPSPASQLAITFLILSLQLGICVMFVVDPSHSVDFODQRTLDPREFARGVLKCDIS	421
DB	690	APRFPSPASQLAITFLILSLQLGICVMFVVDPSHSVDFODQRTLDPREFARGVLKCDMS	749
QY	422	DLSLICLLGYSMLLMWTCTVAIKTRGVPEPFNEAKPIGTMYTTTCIWLAFIPFPFGTS	481
DB	750	DLSLICLLGYSMLLMWTCTVAIKTRGVPEPFNEAKPIGTMYTTTCIWLAFIPFPFGTS	809
QY	482	QSADKLYIQTTTTITSVSLSASVSGLMYPKVYIILLFHPEQNVPKPKRSLKAWTAATM	541
DB	810	QSADKLYIQTTTTITSVSLSASVSGLMYPKVYIILLFHPEQNVPKPKRSLKAWTAATM	869
QY	542	SNKFTOKGNFRNGBAKSCELNLETTPALATKQTIVVTYNHAI	584
DB	870	SNKFTOKGNFRNGBAKSCELNLETTPALATKQTIVVTYNHAI	912

RESULT 15

RECEIVED 13
ADR08623

ID ADR08623

XX
XX

T

AC ADR08623;

XX	
DT	
XX	
XX	04-NOV-2004 (first entry)
DE	
XX	Human protein useful for treating neurological disease Seq 2129.
XX	
KW	human; oligo-capping method; diagnostic marker; gene therapy;
KW	osteoporosis; neurological disease; Alzheimer's disease;
KW	Parkinson's disease; dementia; short memory; cancer;
KW	sense or motor function; emotional reaction; fear response; panic;
KW	osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW	tranquilliser.

xx
OS
Homo sapiens.

[illegible]

PN EP1447413-A2.

XXXXXXXXXXXX

PD 18-AUG-2004.

XX

PF 12-FEB-2004; 2004EP-00003145.

XX
XX
PR
PR
PR
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PA
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PI
PI
PI

14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.

(REAS-) RES ASSOC BIOTECHNOLOGY.

ISOGAI T, YAMAMOTO J, NISHIKAWA T, ISONO Y, SUGIYAMA T, Otsuki T;
WAKAMATSU A, ISHII S, NAQAI K, IRIE R;

XX
DR WPI: 2004-583265/57.
DR N-PSDB; ADR06667.
XX
XX
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1: SEQ ID NO 2129: 2686bp; English.

This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to

cDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the cDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytosstatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-office.

Sequence 591 AA;

Query Match	Score	DB	Length
Best Local Similarity	93.7%	2912.5	591
Matches	96.1%	1.2e-293	
Mismatches	8		
Conservative	13		
Indels			

Qy	3	GVSSSLPTRMT - SGFDRYFSGSRITLNNRRNIWFAEFWEDNFHCKLSHALKKGSHIKCT	61
Db	22	GAVTILPKRMSVGFDRYFSSRTLNNRRNIWFAEFWEDNFHCKLSHALKKGSHVKCT	81
Qy	62	NRERI GODSAYEOBGGKQFVIDAVYANGHALHAMHRDLCPRGVGLCPRMDPVDGTQLLKY	121
Db	82	NRERIGODSAYEOBGGKQFVIDAVYANGHALHAMHRDLCPRGVGLCPRMDPVDGTQLLKY	141
Qy	122	IRNVNFGSIAGNPVTFNENGDA PRGYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERMOWP	181
Db	142	IRNVNFGSIAGNPVTFNENGDA PRGYDIYQYQLRNGSAEYKVIGSWTDHLHLRIERMHP	201
Qy	182	GSQQQLPRSTCSLPCOPGERKKTVMKMACCWHCEPCTGYOYQDRYTKCTCPYDMRPTEN	241
Db	202	GSQQQLPRSTCSLPCOPGERKKTVMKMPCCWHCEPCTGYOYQDRYTKCTCPYDMRPTEN	261
Qy	242	RTSCORPIPIVKLEWDSPAVLPLFLAVVGTAAITLVVVTVFVRVNDTPIVKASGREL SYVL	301
Db	262	RTGCRPIPIIKLEWSPAVLPLFLAVVGTAAITLVVVITFVRVNDTPIVRASGREL SYVL	321
Qy	302	LAGIFLCYATTFMLIAEPDLGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSVS	361
Db	322	LAGIFLCYATTFMLIAEPDLGTCSLRRI FLGLGMSISYAALLTKTNRIYRIFEQGKRSVS	381
Qy	362	APRFSPASQIATTFILISQLLIGICWFFVVDSSHVSVDQDORTLDPFRARGVCLKDIS	421
Db	382	APRFSPVSQIATTFILISQLLIGICWFFVVDSPSHVLDQDORTLDPFRARGVCLKDIS	441
Qy	422	DLSLICLLGYSMLLMWTCTVYAIKTRGVPTFNEAKPIGFTMTWTTICLVWLAFTPIFPGTS	481
Db	442	DLSLICLLGYSMLLMWTCTVYAIKTRGVPTFNEAKPIGFTMTWTTICLVWLAFTPIFPGTS	501
Qy	482	QSDAKLYIQTTTLITVSVLSASVSLGMLNPKVYIILFHPSEQNVPRKRSLKAVVTAATM	541
Db	502	QSDAKLYIQTTTLITVSVLSASVSLGMLNPKVYIILFHPSEQNVPRKRSLKAVVTAATM	561
Qy	542	SNKPTOKGNPRPNGEAKSELCEMLETP	568
Db	562	SNKPTOKGNPRPNGEAKSELCEMLEAP	588

Search completed: June 17, 2005, 18:14:23
Job time : 173 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 17, 2005, 18:19:18 ; Search time 315.5 Seconds

(without alignments)

5696.982 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 3303

Sequence: 1 atgcacggggatcatcatc.....acacaaaccatgccatctag 1755

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cpn2.1/USPTO spool_p/US10828332/runat 17062005 171336 24951/app query.fasta_1.1927
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10828332 @CNC 1.1 354 @runat 17062005 171336 24951 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	92.4	912	1 MGR4 RAT	P31423 rattus norv
2	2004.5	91.0	912	1 MGR4_HUMAN	Q14833 homo sapien
3	2752.5	83.3	796	2 Q6ZMQ2	Q6ZMQ2 homo sapien
4	2732	82.7	983	2 Q6Z916	Q6Z916 rattus norv
5	2546.5	77.1	832	2 Q6BEF4	Q6BEF4 mus musculus
6	2377	72.0	908	1 MGR8_HUMAN	O00222 homo sapien
7	2377	72.0	908	2 Q6B964	Q6B964 mus musculus
8	2371	71.8	908	1 MGR8 RAT	P70579 rattus norv
9	2336	70.7	908	1 MGR8_MOUSE	P47743 mus musculus
10	2219	67.2	915	1 MGR7_HUMAN	Q14831 homo sapien
11	2214	67.0	915	2 Q6BED2	Q6BED2 mus musculus
12	2210	66.9	915	1 MGR7 RAT	P35400 rattus norv
13	2189	66.3	906	2 Q8NFS2	Q8NFS2 homo sapien
14	2189	66.3	911	2 Q8NFS3	Q8NFS3 homo sapien
15	2189	66.3	924	2 Q8NFS4	Q8NFS4 homo sapien
16	2111.5	63.9	551	2 Q9PWQ0	Q9PWQ0 fugu rubrip

17	2069.5	62.7	680	2 Q76MR0	Q76MR0 poephila gu
18	2054	62.2	877	1 MGR6_HUMAN	Q15303 homo sapien
19	2045.5	61.9	868	1 Q863I4	Q863I4 oryctolagus
20	2026.5	61.4	871	1 MGR6 RAT	P35349 rattus norv
21	1967.5	59.6	546	2 Q8CFQ7	Q8CFQ7 mus musculus
22	1962.5	59.4	977	2 Q9PWE1	Q9PWE1 ictalurus p
23	1855	56.2	620	2 Q76E43	Q76E43 poephila gu
24	1284.5	38.9	1520	2 Q8NHA9	Q8NHA9 homo sapien
25	1240.5	37.6	976	1 MGR DROME	P91685 drosophila
26	1223.5	37.0	780	2 Q7KQ59	Q7KQ59 drosophila
27	1223.5	37.0	1073	2 Q7OGQ8	Q7OGQ8 drosophila
28	1223.5	37.0	1226	2 Q9V4U3	Q9V4U3 drosophila
29	1223.5	37.0	1264	2 Q9V4U4	Q9V4U4 drosophila
30	1181	35.8	933	2 Q75QW7	Q75QW7 apis mellif
31	1179	35.7	843	2 Q6S738	Q6S738 apis mellif
32	1171.5	35.5	872	1 MGR2 RAT	P31421 rattus norv
33	1155.5	35.0	877	1 MGR3_HUMAN	Q14832 homo sapien
34	1155.5	35.0	879	1 MGR3_MOUSE	Q9GY82 mus musculus
35	1155.5	35.0	879	2 Q86YG6	Q86YG6 homo sapien
36	1152.5	34.9	879	1 MGR3 RAT	P31422 rattus norv
37	1150.5	34.8	872	1 MGR2_HUMAN	Q14416 homo sapien
38	1148.5	34.8	877	2 Q8TBH9	Q8TBH9 homo sapien
39	1148.5	34.8	1040	2 Q75QW6	Q75QW6 apis mellif
40	1129	34.2	1194	1 MGR1_HUMAN	Q13255 homo sapien
41	1123	34.0	942	2 Q6J164	Q6J164 homo sapien
42	1123	34.0	1212	1 MGR5_HUMAN	P41594 homo sapien
43	1122	34.0	1156	2 Q98UC6	Q98UC6 gallus gall
44	1122	34.0	1188	2 Q98UC5	Q98UC5 gallus gall
45	1122	34.0	1199	1 MGR1 RAT	P23385 rattus norv

ALIGNMENTS

RESULT 1

MGR4 RAT
ID MGR4 RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 4 precursor (mGluR4).
DE Name=Gm4; Synonyms=Gprcid, Mglur4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93332699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thoenes H., Venezia D., Haldeman B.A.,
RA McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
RN [3]
RP INTERACTION WITH PRKCBP.
RX MEDLINE=20571397; PubMed=1112333;
RA El Far O., Alras J., Wischmeyer E., Nehring R.B., Karschin A.,
RA Betz H.;
RT "Interaction of the C-terminal tail region of the metabotropic
glutamate receptor 7 with the protein kinase C substrate PICK1.";
RL Eur. J. Neurosci. 12:4215-4221(2000).
CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is
mediated by a G-protein that inhibits adenylyl cyclase activity.
CC -!- SUBUNIT: Interacts with PRKCBP.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Is widely distributed in the CNS. Predominant
 CC expression is seen in the granule cells of the cerebellum.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
 CC -----
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 CC -----

DR EMBL; M92077; -; NOT ANNOTATED_CD.
 DR EMBL; M90518; AAA93190.1; -.
 DR PIR; JH0563; JH0563.
 DR HSSP; P23385; LEWK.
 DR RGD; 2745; Grm4.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Metglu_receptor.
 DR InterPro; IPR001786; Metglu_receptor4.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF receptor; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 DR G-protein coupled receptor; Glycoprotein; Multigene family; Signal;
 KW Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 912 Metabotropic glutamate receptor 4.
 FT DOMAIN 33 587 Extracellular (Potential).
 FT TRANSMEM 588 610 1 (Potential).
 FT DOMAIN 611 624 Cytoplasmic (Potential).
 FT TRANSMEM 625 645 2 (Potential).
 FT DOMAIN 646 656 Extracellular (Potential).
 FT TRANSMEM 657 675 3 (Potential).
 FT DOMAIN 676 699 Cytoplasmic (Potential).
 FT TRANSMEM 700 720 4 (Potential).
 FT DOMAIN 721 750 Extracellular (Potential).
 FT TRANSMEM 751 772 5 (Potential).
 FT DOMAIN 773 785 Cytoplasmic (Potential).
 FT TRANSMEM 786 808 6 (Potential).
 FT DOMAIN 809 821 Extracellular (Potential).
 FT TRANSMEM 822 847 7 (Potential).
 FT DOMAIN 848 912 Cytoplasmic (Potential).
 FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 454 454 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 569 569 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 124 124 Q -> R (in Ref. 2).
 SQ SEQUENCE 912 AA; 101818 MW; 336430EF19B4B577 CRC64;

Alignment Scores:

Pred. No.: 5,848-174 Length: 912
 Score: 3050.50 Matches: 575
 Percent Similarity: 98.97% Conservative: 2
 Best Local Similarity: 98.63% Mismatches: 5
 Query Match: 92.36% Indels: 1
 DB: 1 Gaps: 1

US-10-828-332-6 (1-1755) x MGR4_RAT (1-912)

QY 7 GGGGTATCATCATCTTTGCCACGAGGATGACA---TCAGGGTTCCGACCGATCTTCTCC 63
 Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCGACGCTGGACACACAGCGCGCAACATCTGTTTGGCGAGTCTTGGGAGGACAAAC 123
 Db 350 SerArgThrLeuAspAsnArgAsnIleTyrPheAlaGluPheTyrGluAspAsn 369

QY 124 TTCCATTGCAAGTTGAGCGCCACGCGCTCAAGAAAGGAGCCACATCAAGAAGTGACCC 183
 Db 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisLleLysLysCysThr 389
 QY 184 AACCCAGAGCGCATCGGGCAGGACTCGCCCTATCAGCAGGAGGGGAAAGTGCAGTCTGTG 243
 Db 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
 QY 244 ATTGACCGCTGTAGCCATCGGGCAGCGCTGCACGCCATGCACCGTGCAGCTGTGTC 303
 Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GCGCGCTAGGACTCTGCGCTCGCATGGACCCCGTGGATGGCACCACAGCTCTTAAAGTAC 363
 Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGGAACGTCAACTTCTCAGGCATTGCGGGGAACCTGTAACTTCAATGAAACCGA 423
 Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GACCCACGGGGCGCTACGACATCTACAGTACCACTGCGCAATGGCTGCGCGAGTAC 483
 Db 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 489
 QY 484 AAGTCTCATCGCTCGTGACAGACACCTGCACCTCAGAAATAGAGCGGATGCAGTGGCCA 543
 Db 490 LysValIleGlySerThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 509
 QY 544 GGGAGTGGCCACGACGCTGCGCGCTCCATCTGCAGTCTGCCCTCCACGCCGCGGAGCGA 603
 Db 510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAAGCTGTGAAGGCGATGGCTTGTCTGGCACTGCGAGCCCTGCACCGGTACCAG 663
 Db 530 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATGCGGCCCCACAGAGAAC 723
 Db 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGAGTGCACGACCCATCCCATCGTCAAGTTGGAGTGGAGCTGCGCTGCGGCGGTG 783
 Db 570 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 589
 QY 784 CTGCGCTCTTCTTGGCGGTGGTGGCATCGCCGCGCAGCTGTTGCTGGTGTGCACGTTT 843
 Db 590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 609
 QY 844 GTGCGCTACCAACGATACCCCATCGTCAAGCGCTCGGGCCGGGAACCTGAGCTAGTGTCTG 903
 Db 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
 QY 904 CTGCGCGGCGCATCTTTCTGTGTGTACGCCACTACCTTCCTCATGATCGCAGACCGGACCTG 963
 Db 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
 QY 964 GGGACCTGTTGCTTCCGCGCGCATCTTCTAGGGCTCGGCATGACATCAGCTACGCGGCC 1023
 Db 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
 QY 1024 CTGCTGACCAAGCAACCGCATTTTACCGCATCTTTTGGACGAGGGCAACCGTCCGTCACT 1083
 Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
 QY 1084 GCCCGCGCTTTCATCAGCCCGCGCTCGCAGCTGCCATCACCTTCATCTCATCTTCCCTG 1143
 Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 709
 QY 1144 CAGCTGCTCGGCATCTCGCTGT 1203
 Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729

QY 1204 CAGGACCAACGACACTTGCACCCCGCTTTCAGGGGCGTCTCAAGTGCACATCTCG 1263
DB 730 GlnAseGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY 1264 GACCTGTCTCCTCATCTGCTGCTGGGCTACAGCATGCTGCTGATGTCACGTGTACTGTG 1323
DB 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TAGCCCATCAAGACCCGAGCGGTGCCCGAGACTTCAACAGGCGCAAGCCCATCGCTTC 1383
DB 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACATGTCATCAACCACTGCTGCTGGCTGGCTTCATCCCATCTTTTTCGCCACTCA 1443
DB 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
QY 1444 CAGTCAGCCGACAAAGCTGTACATCCAGACACACACTCACGCTCTCCGTGAGTGTGAGC 1503
DB 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
QY 1504 GTTTCAGTCTCCCTGGGATGCTTACATGCCCAAGTTCATCATCTCTTCCACCGC 1563
DB 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
QY 1564 GAGCAGAAGCTGCCAGCGGAGCGGAGCTCTCAAGCCGCTGTCACGCCGCCACCATG 1623
DB 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
QY 1624 TCCAAACAGTTCACAGAGGCGCACTTCAGSCCAATGGGAGGCAAGCAATCAGAGCTG 1683
DB 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACCTGGAGACCCAGCGCTGGCTACCAACAGACCTAGCTCACCTACACCAAC 1743
DB 890 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
QY 1744 CATGCCATC 1752
DB 910 HisAlaIle 912

RESULT 2
MGR4_HUMAN
ID MGR4_HUMAN STANDARD; PRT; 912 AA.
AC Q14833;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 4 precursor (mGluR4).
GN Name=GRM4; Synonyms=GPRC1D, MGLUR4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96346635; PubMed=8738157; DOI=10.1016/0169-328X(95)00321-I;
RA Makoff A., Lechuk R., Oker M., Harrington K., Emson P.;
RT "Molecular characterization and localization of human metabotropic
glutamate receptor type 4.";
RL Brain Res. Mol. Brain Res. 37:239-248 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98141892; PubMed=9473604; DOI=10.1016/S0169-328X(97)00277-5;
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
RA Rosbeck P.R. Jr., Johnson B.G., Schoep D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
molecular cloning, functional expression, and comparison of
pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

MEDLINE=95342351; PubMed=7617140; DOI=10.1016/0028-3908(94)00149-M;
Flor P.J., Lukic S., Rueegg D., Leonhardt T., Knoepfel T., Kuhn R.;
RT "Molecular cloning, functional expression and pharmacological
characterization of the human metabotropic glutamate receptor type
4.";
RL Neuropharmacology 34:149-155 (1995).
RN [4]
RP VARIANT ILS-797.
MEDLINE=21416233; PubMed=11525421;
RX Ohtsuki T., Toru M., Arinami T.;
RT "Mutation screening of the metabotropic glutamate receptor mGluR4
(GRM4) gene in patients with schizophrenia.";
RL Psychiatr. Genet. 11:79-83 (2001).
CC -!- FUNCTION: Receptor for glutamate. The activity of this receptor is
mediated by a G-protein that inhibits adenylyl cyclase activity.
CC -!- SUBUNIT: Interacts with PRKCAP (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Strongly expressed in the cerebellum.
CC Expressed at low levels in hippocampus, hypothalamus and thalamus.
CC No expression detected in liver.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X80818; CA56784.1; -;
CC EMBL; U92457; AAB51762.1; -;
CC HSSP; P23385; LEWK.
CC Genew; HGNC:4596; GRM4.
CC MIM; 604100; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . . ; TAS.
CC GO; GO:0007194; P:negative regulation of adenylyl cyclase ac. . . ; TAS.
CC GO; GO:0007268; P:synaptic transmission; TAS.
CC InterPro; IPR001828; ANF receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC InterPro; IPR000162; Mglu_receptor.
CC InterPro; IPR001786; Mglu_receptor4.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF receptor; 1.
CC PRINTS; PR00248; GPCR_MGR.
CC PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
CC PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
CC G-protein coupled receptor; Glycoprotein; Multigene family;
KW Polymorphism; Signal; Transmembrane.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 912 Metabotropic glutamate receptor 4.
FT DOMAIN 33 587 Extracellular (Potential).
FT TRANSMEM 588 610 1 (Potential).
FT DOMAIN 611 624 Cytoplasmic (Potential).
FT TRANSMEM 625 645 2 (Potential).
FT DOMAIN 646 656 Extracellular (Potential).
FT TRANSMEM 657 675 3 (Potential).
FT DOMAIN 676 699 Cytoplasmic (Potential).
FT TRANSMEM 700 720 4 (Potential).
FT DOMAIN 721 750 Extracellular (Potential).
FT TRANSMEM 751 772 5 (Potential).
FT DOMAIN 773 785 Cytoplasmic (Potential).
FT TRANSMEM 786 808 6 (Potential).
FT DOMAIN 809 821 Extracellular (Potential).
FT TRANSMEM 822 847 7 (Potential).
FT DOMAIN 848 912 Cytoplasmic (Potential).
FT CARBOHYD 98 98 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 301 301 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 454 454 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 484 484 N-linked (GlcNAc . .) (Potential).

OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK131536; BAD18673.1;
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0008067; F-metabotropic glutamate, GABA-B-like recepto...; IEA.
 DR GO; GO:0004872; F-receptor activity; IEA.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Mrglu_receptor.
 DR InterPro; IPR001786; Mrglu_receptor4.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR00593; MTABOTROPICR.
 DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PROSITE; PS00259; G_PROTEIN_RECP_F3_4; 1.
 KW Receptor.
 SQ SEQUENCE 796 AA; 88492 MW; FAE466D1D45D3829 CRC64;

Alignment Scores:
 Pred. No.: 3,61e-156 Length: 796
 Score: 2752.50 Matches: 530
 Percent Similarity: 92.20% Conservative: 14
 Best Local Similarity: 89.83% Mismatches: 38
 Query Match: 83.33% Indels: 8
 DB: 2 Gaps: 3

US-10-828-332-6 (1-1755) x Q62MQ2 (1-796)

QY 3 GCACGGGTATCATCATCTTCCACAGAGGATGACATCAGGGTTCGACGATCTCTC 62
 DB 209 AlaArgAlaValIlePheAlaAsnGluAspIleArg---ArgValLeu-GluAl 227
 QY 63 CAGCCGACGCTGGACAACAACAGCGCCACATCTGTTT---GCCAGTCTCTGGAGGA 119
 DB 227 alaArgArgAlaAsnGlnThrGlyHisPhePheTrpMetGlySerAspSerTrpGlySe 247
 QY 120 CAATTCATTCAGAGTTCAGCGCCACCGCGCTCAAGAGGAGGAGC----- 165
 DB 247 rLysIleAlaProValLeuHisLeuGluGluValAlaGluGlyAlaValThrIleLeuPr 267
 QY 166 -CACATCAAGAGTGACCAACAGGAGGCGATCGGGCAGGACTCGGCCTATGACAGGA 224
 DB 267 oLysArgMetSerValArgAspArgGluArgIleGlyGlnAspSerAlaIleGlnG 287
 QY 225 GGGGAAGTGCAGTTCGTCATTCACGCTGTGTACGCTATGGCCATGGCCCGCTCGACGCCAT 284
 DB 287 uGlyValGlnPheValIleAspAlaValTrpAlaMetGlyHisAlaLeuHisAlaMe 307
 QY 285 GCACCGTACCTGTGTCCCGCGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGATGG 344
 DB 307 thsArgAspLeuCyseProGlyArgValGlyLeuCyseProArgMetAspProValAspGl 327
 QY 345 CACCCAGCTCTTACGTACATCAGGACGTCACCTCTCAGGCATTCGGGGACCCCTGT 404
 DB 327 yThrGlnLeuLeuLysIleArgAsnValAsnPheSerGlyIleAlaGlyAsnProVa 347
 QY 405 AACCTTCAATGAAACGAGAGCGACCGGGCGCTACGACATCTACAGTACCAACTGGG 464
 DB 347 lThrPheAsnGluAsnGlnAspAlaProGlyArgTrpAspIleTrpGlnThrGlnLeuAr 367
 QY 465 CAATGGCTCGCGGAGTACAAGGTATCATCGGCTCATCGGTGGACAGACCACTGACCTCAGAA 524

DB 367 GAenAaspSerAlaGluTrpLysValIleGlySerTrpThrAspHisLeuHisLeuArgIl 387
 QY 525 AGACGGGATGATGAGTCCGAGGAGTGGCCAGAGTGGCCGCGCTCCATCTGCAGTCTGCC 584
 DB 387 eGluArgMetHisTrpProGlySerGlyGlnGlnLeuProArgSerIleCysSerLeuPr 407
 QY 585 CTGCAGCCCGGGAGAGCAAGAACAGTGTGAAGGCGATGGCTTGTCTGCTGGCAGTCCGA 644
 DB 407 oCyseGlnProGlyGluArgLysLysThrValLysGlyMetProCyseCysTrpHisCysGl 427
 QY 645 GCCTTCGACCCGGGTACCAAGTGCAGCGCTACACCTCTAAGACCTGCCCTTACCA 704
 DB 427 uProCysThrGlyTrpGlnTrpGlnValAspArgTrpThrCysLysThrCysProTrpAs 447
 QY 705 CATGCGGCCACAGAGAACCGCACGAGCTGCCAGCCCATCCCATCTGCAGTCTGGAGTG 764
 DB 447 pMetArgProThrGluAsnArgThrGlyCysArgProIleProIleLeuLeuGluTr 467
 QY 765 GAGCTCGCGTGGCGGCTGCTGCCCTCTTCTCGCGGTGGGGATCGCGCCACGCT 824
 DB 467 pGlySerProTrpAlaValLeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLe 487
 QY 825 GTTCGTGTGTGTACGTTTGTGCGCTACAAAGATACCCCATCTGCAGGCGCTCGGGCG 884
 DB 487 uPheValIleThrPheValArgTrpAsnAspThrProIleValLysAlaSerGlyAr 507
 QY 885 GGAACCTGAGCTACGTGCTGGCGGCGATCTTCTGTGCTACGCGCATCTTCTCAT 944
 DB 507 gGluLeuSerTrpValLeuLeuAlaGlyIlePheLeuCyseTrpAlaThrThrPheLeuMe 527
 QY 945 GATCCGAGCGGACCTGTGGGAGCTGTTCGCTCCGCGCATCTTCTTAGGCTCGGCAT 1004
 DB 527 tileAlaGluProAspLeuGlyThrCysSerLeuArgIlePheLeuGlyLeuGlyMe 547
 QY 1005 GAGCATCAGTACCGCGGCTGCTCACCAGCAACCGCATTTACCGCATCTTTGAGCA 1064
 DB 547 tSerIleSerTrpAlaAlaLeuLeuThrLysThrAsnArgIleTrpArgIlePheGluGl 567
 QY 1065 GGGCAAAACGGTTCAGTGGCCCGCTTTCATCAGCCGCGCTCGCAGTCCGCATCAC 1124
 DB 567 nGlyLysArgSerValSerAlaProArgPheIleSerProAlaSerGlnLeuAlaIleTh 587
 QY 1125 CTTCATCTCATCTCCCTGCGAGCTGCTCGGCATCTCGGTGTGGTGTGGTGGAGCCCTC 1184
 DB 587 rPheSerLeuIleSerLeuGlnLeuGlyIleCyseValTrpPheValValAspProSe 607
 QY 1185 CCATCTCGTGTGGTTCAGGACCAAGGACATTCACCCCGCTTTCGAGGGCGT 1244
 DB 607 rHisSerValValAspPheGlnAspGlnArgThrLeuAspProArgPheAlaArgGlyVa 627
 QY 1245 GCTCAAGTGCACATCTCGACCTGCTCCTCATCTGCTGCTGGGCTACAGCATCTGCT 1304
 DB 627 lLeuLysCysAspIleSerAspLeuSerIleLeuLeuGlyTrpSerMetLeuLe 647
 QY 1305 GATGTCACGTGTACTGTGTAGCGCATCAAGACCGGCGGTGGCCGAGACCTTCAACGA 1364
 DB 647 uMetValThrCysThrValTrpAlaIleLysThrArgGlyValProGluThrPheAsnGl 667
 QY 1365 GGCMAAGCCCATCGCTTACCATGTATACACCTGCAATGCTGCTGGCTGGCTTATCCC 1424
 DB 667 uAlaLysProIleGlyPheThrMetTrpThrCysIleValTrpLeuAlaPheIlePr 687
 QY 1425 CATCTTTTTCGACCTCACAGTACGCGACAGGTGTACATCCAGACCAACACCACTGAC 1484
 DB 687 oIlePhePheGlyThrSerGlnSerAlaAspLysLeuTrpIleGlnThrThrLeuTh 707
 QY 1485 GGTCTCCGTGAGTCTGAGCGCTTACGTCTCCCTGGGGATGTCTATCATGCCCAAGTCTA 1544
 DB 707 rValSerValSerLeuSerAlaSerValSerLeuGlyMetLeuTrpMetProLysValTy 727
 QY 1545 CATCATCTTTCACCCCGGAGCAACGTGCCCGCAAGCGGAGCTCTCAAGCGCT 1604

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Db      727 r1e1leLeuPheHisProGluGlnAsnValProLysArgLysArgSerLeuLysAlaVal 747
Qy      1605 GGTACCCCGCCACCATGTCACAAAGTTCACACAGAGGCGCACTTCAGGCCCAATGG 1664
Db      747 lValThrAlaAlaThrMetSerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGI 767
Qy      1665 GAAAGCCCAATCAGAGCTGTGTGAGAACTTGAGACCCCGCTGGCTATCAACAACAGAC 1724
Db      767 yGluAlaLysSerGluLeuCysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnTh 787

Qy      1735 TCATCTACCTACACCAACCATGCCATC 1752
Db      787 rTyrValThrTyrThrAsnHisAlaIle 796

RESULT 4
Q62916 PRELIMINARY; PRT; 983 AA.
AC Q62916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Metabotropic glutamate receptor 4b..
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47331; AAA88788.1; -.
DR HSSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000162; Mtglu_receptor.
DR InterPro; IPR001786; Mtglu_receptor4.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMGR.
DR PRINTS; PR01054; MTABOTROP4R.
DR PRINTS; PR00593; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;

Alignment Scores:
Pred. No.: 6,26e-155 Length: 983
Score: 2732.00 Matches: 535
Percent Similarity: 85.09% Conservative: 7
Best Local Similarity: 83.99% Mismatches: 34
Query Match: 82.71% Indels: 61
DB: 2 Gaps: 7

US-10-828-332-6 (1-1755) x Q62916 (1-983)
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Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
Qy 64 AGCCCGACGCTGACCAACAGCGCGCAACATCTGGTTGCCAGTCTCTGGGAGGACAAAC 123
Db 350 SerArgThrLeuAspAsnAsnArgAsnIleThrPheAlaGluPheTrpGluAspAsn 369
Qy 124 TTCCCATTCGAAGTTGAGCGCGCACCGCTCAAGAAAGGGAAGCCACATCAAGAAGTGACCC 183

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Db      370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLeuLysCysThr 389
Qy      184 AACCGAGAGCGCATCGGSCAGGACTCGGSCCTATCAGCAGAGGAGGGAAGGTCCAGTTCGTG 243
Db      390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
Qy      244 ATTGACCGCTGTGTACGCCATCGGCGCACCGCTGCACGCCCATGCACCGTGACCTGTGTCCC 303
Db      410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
Qy      304 GGCCCGTAGGACTCTGCTCCCTCGCATGAGCCCGTGTGATGCGCACCACCGAGCTCTTAAGTAC 363
Db      430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
Qy      364 ATCAGGAACGTCAACTTCTCAGGCATTGCGGGGAACCTGTAACTTCAATGAGAACGGA 423
Db      450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
Qy      424 GACGCACCGGCGCTACGACATCTACCACTTACCACTGCGCAATGGCTCGGCCGAGTAC 483
Db      470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr 489
Qy      484 AAGTCAATCGGCTCGTGGACAGACCATCTGCACCTCAGATAGAGCGGATGACGTGGCCA 543
Db      490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 509
Qy      544 GGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCGCGGAGCGA 603
Db      510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
Qy      604 AAGAAGACTGTGAAGGCGCTGCTGCTGCGCACTGCGAGCCCTGCACCGGTTACCAAG 663
Db      530 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrGln 549
Qy      664 TACCAAGTGAACCGCTACACTGTAAAGCTGCCCCCTACGACATCGCGGCCACAGAGAAC 723
Db      550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
Qy      724 CGCAGGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGCTGGCGCTG 783
Db      570 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 589
Qy      784 CTGCCCCCTCTTCTGGCGCTGGTGGGATCGCCCGCACGCTGTTCTGGTGGTGCACGTTT 843
Db      590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 609
Qy      844 GTGGCTTACAAAGATACCCCATCTCGTCAAGCCCTGGCGCGGAGAACTGAGTACGTGCTG 903
Db      610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
Qy      904 CTGGCGGCGCATCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 963
Db      630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
Qy      964 GGGACCTGTTCTCGCTCCCGCATCTTCTAGGGCTCGGCGCATGAGCATCAGCTACGCGGCC 1023
Db      650 GlyThrCysSerLeuArgGlyIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
Qy      1024 CTGCTGACCAAGACCAACCGCATTTACGGCATCTTTGAGGAGGCGCAACCGTGGTCACT 1083
Db      670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
Qy      1084 GCCCGCGTTTCATCAGCCGCGCTCGCAGCTGGCCCATCACCTTCATCTCTCTCCCTG 1143
Db      690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 709
Qy      1144 CAGTGTCTCGGCATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1203
Db      710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
Qy      1204 CAGACCAACAGGACACTTGTACCCCGCTTTCAGGAGGCGGTGTCAAGTGGACATCTCG 1263
Db      730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749

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QY 1264 GACCTCTCCTCATCTGCTGCTGGCTACAGCATCTCTGATGTCACGTGACTGTG 1323
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 QY 1324 TAGCGCATCAAGACCGCGCTGCCGAGACCTTCAACGAGCGCCCAAGCCATCGGCTTC 1383
 DB 770 TyrAlaIleuSerThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
 QY 1384 ACCATGTACACCACTGCTGCTGCTGGCTTTCATCCCATCTCTTTTGGCAGCTCA 1443
 DB 790 ThrMetTyrThrThrCysIleValTTPLeuAlaPheIleProIlePheGlyThrSer 809
 QY 1444 CAGTCAGCGCAGCAAGCTGTACATCTCAGACCAACCACTGACGGTCTCTCGTGTGAGC 1503
 DB 810 GinSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GCTTCAGTCTCCTGGGATGCTTACATGCCCAAGTCTACATCATCTCTCTTCCAC--- 1560
 DB 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisIle 849
 QY 1561 ---CCGAGCAGAACGTCGCCCAAGCGCAGTCTCAAGCGCGTCTCAAGCGCGCC 1617
 DB 850 PhePro-PheCysSerTyrProSer-----ProAlaIleCysProAl 863
 QY 1618 ACATGTCCCAACAGT-----AGAGGGCAACTTCAGGCCCAATGGGAAGCCAAATCA 1677
 DB 903 sValAlaLysGluLysLysGlyGlyGlySerProProThrLysLysProlsGly 923
 QY 1678 G-----AGCTGTGTGAGAACCTCGAGACCCAG----- 1705
 DB 923 nlysLeuIleLeuSerValPheArgSerAlaAlaSerTyrTyrProValCysProC 943
 QY 1706 -CGTGGCTACCAACAGACCTACGTACCTACACCAACCATGCCATCT 1753
 DB 943 sGlyLeuGlnProAlaArgProProTyrProSerAlaValCysProAla 959
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 Q68EF4
 ID Q68EF4 PRELIMINARY; PRT; 832 AA.
 AC Q68EF4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodargren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RA Director MGC Project;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC080284; AAH80284.1; -;
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Mtblu_receptor.
 DR InterPro; IPR001786; Mtblu_receptor4.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR01054; MTABOTROPICAR.
 DR PRINTS; PR00593; MTABOTROPICAR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 832 AA; 92832 MW; 2B90570F77861FB1 CRC64;
 Alignment Scores:
 Pred. No.: 7,35e-144 Length: 832
 Score: 2546.50 Matches: 477
 Percent Similarity: 96.41% Conservative: 6
 Best Local Similarity: 95.21% Mismatches: 17
 Query Match: 77.10% Indels: 1
 DB: 2 Gaps: 1
 US-10-828-332-6 (1-1755) x Q68EF4 (1-832)
 QY 7 GGGGTATCATCATCTTTGCCAACGAGATGACA---TCAGGGTTCCAGCGATACCTTCTCC 63
 DB 330 GlyAlaValThrIleLeuProLysArgThrSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCCGCAGCTGGCAACAACAGCGCAACATCTGTTTCCGAGTCTCTGGAGGACAC 123
 DB 350 SerArgThrLeuAspAsnAsnArgAsnIleTyrPheAlaGluPheTyrGluAspAsn 369
 QY 124 TTCCATTGCAAGTTGAGCGCCGCGCTCAAGAGGAAGCCACATCAAGAAGTGACCC 183
 DB 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysCysThr 389
 QY 184 AACCGAGAGCGCATCGGCGAGACTCGGCCCTATGACGAGGAGGGAAGGTGCGATTCTGG 243
 DB 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
 QY 244 ATTGAGCTGTGTAGCCCATGGCCACCGCTGCACCGCATGCCGCTGACCTGTGTC 303
 DB 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GGCCGCTAGGACTCTGCGCTCGCATGGACCCCGGTGGATGGCACCCAGCTGCTTAAGTAC 363
 DB 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGGAACGTCAACTTCTCAGGCATTCGCGGGAACCTGTAACTTCAATGAGAACGGA 423
 DB 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 CAGCAGCGGGCGCTACGACATCTACAGTACCACTGCGCACTGGCTCGGCCGAGTAC 483
 DB 470 AspAlaProGlyArgTyrAspIleTyrGlnArgArgAsnGlySerAlaGluTyr 489


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QY 484 AAGTCATCGCTCGTGACACAGACACCTGACCTCAGATAGAGCGGATCGATGCGCA 543
Db 490 LysValIleGlySerTrpThrAspHisLeuArgIleGluArgMetGlnTrpPro 509
QY 544 GGGAGTGCCAGACAGCTCCGCGCTCCATCTGCAGCTCGCCCTCCAGCCCGGGAGCGCA 603
Db 510 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
QY 604 AAGAGACTGTGAAGGGCATGCTGTGCTGGACACTCGAGCCCTGCACCGGGTACGAG 663
Db 530 LysIleThrValIleGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTrpGln 549
QY 664 TACCAGTGGGCGCTACACCTGTAAAGACCTGCCCTACGACATCGCGCCACACAGAAC 723
Db 550 TyrGlnValAlaAspArgTyrThrCysIleThrCysProTyrAspMetArgProThrGluAsn 569
QY 724 CGCAGAGCTGCCAGCCCATCCCATCTCAAGTTGGAGTGGGACTCCCGCTGGCGCGTG 783
Db 570 ArgThrSerCysGlnProIleProIleValIleLysLeuGluTrpAspSerProTrpAlaVal 589
QY 784 CTGCCCTCTTCCTGGCGGTGGGCATCGCCGACGCTGCTCGTGGTGGTCACTGTTT 843
Db 590 LeuProLeuPheLeuAlaValIleGlyIleAlaAlaThrLeuPheValValValThrPhe 609
QY 844 GTGCGCTACAGCATACCCCATCGTCAAGCCCTCGGCGCGGAGTGAAGTACTAGTGTG 903
Db 610 ValArgTyrAsnAspThrProIleValIleLysAlaSerGlyArgGluLeuSerTyrValLeu 629
QY 904 CTGGCGGCGCATCTTCTGTGCTACGCCACTACCTTCCTCATGATCGAGCGCGGACCTG 963
Db 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
QY 964 GGGACCTGTTCCTCGCTCCGCGCATCTTCCTAGGGCTGGCATGAGCATCAGTACGCGCC 1023
Db 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
QY 1024 CTGCTGACACAGACCAACCGCATTTACCGCATCTTTGACGAGGGCAACGGTGGTCAGT 1083
Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
QY 1084 GCCCGCGCTTTCATCAGCGCGGCTCGCAGCTGGCCATCCTCATCTCATCTCCCTG 1143
Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheValLeuIleSerLeu 709
QY 1144 CAGTGTCTCGCATCTCGTGTGGTTCGTGTGGACCCCTCCCATCTCGTGGTGGACTTC 1203
Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY 1204 CAGGACCAACGACACTTGACCCCGCTTCCAGGGGGGTGCTCAAGTGGACATCTCG 1263
Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY 1264 GACCTGTCCCTCATCTGCTGTGGCTACAGCATGCTGCTGATGGTCACTGCTACTGTG 1323
Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TACGCCATCAAGACCCGAGGGGTGCCCGAGACCTTCAACGAGGGCAACCCCATCGGCTTC 1383
Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACCATGTACACCATCTGCTGCTGGCTGGCTTCACTCCCATCTCTTTTGGCACCTCA 1443
Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
QY 1444 CAGTCAGCGGACAGCTGTACATCCAGCAACACACACTGACGGTCTCGTGGTCTGAGC 1503
Db 810 GlnSerAlaAspLysValThrSerGluAlaLeuProValGluPheSerProProLeuLeu 829
QY 1504 GCT 1506
Db 830 Ala 830
```

RESULT 6

MGR8_HUMAN STANDARD; PRT; 908 AA.

AC 000222; OLS493; O95945; O95946;

DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Metabotropic glutamate receptor 8 precursor (mGluR8).

GN Name=GRM8; Synonyms=GPCR1H, MGLUR8;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A. (ISOFORM A).

MEDLINE=98141892; PubMed=9473604; DOI=10.1016/S0169-328X(97)00277-5;

Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,

Rothstein P.R. Jr., Johnson B.G., Schoepf D.D., Belagaje R.M.;

"Group III human metabotropic glutamate receptors 4, 7 and 8:

molecular cloning, functional expression, and comparison of

pharmacological properties in RGT cells.";

Brain Res. Mol. Brain Res. 53:88-97(1998).

[2]

SEQUENCE FROM N.A. (ISOFORM A).

MEDLINE=97446143; PubMed=9299241; DOI=10.1006/geno.1997.4842;

Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.-C.;

"The human metabotropic glutamate receptor 8 (GRM8) gene: a

disproportionately large gene located at 7q31.3-q32.1.";

Genomics 44:232-236(1997).

[3]

SEQUENCE FROM N.A. (ISOFORMS B AND C).

TISSUE=Petal brain;

MEDLINE=99234274; PubMed=10216218; DOI=10.1016/S0169-328X(99)00050-9;

Malherbe P., Kratzelstein C., Lundstrom K., Richards J.G., Faull R.L.M.,

Mutel V.;

"Cloning and functional expression of alternative spliced variants of

the human metabotropic glutamate receptor 8.";

Brain Res. Mol. Brain Res. 67:201-210(1999).

-1- FUNCTION: Receptor for glutamate. The activity of this receptor is

mediated by a G-protein that inhibits adenylyl cyclase activity.

-1- SUBUNIT: Interacts with PRKCAP (By similarity).

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;

Name=A; Synonyms=mGluR8a;

Isoid=000222-1; Sequence=Displayed;

Name=B; Synonyms=mGluR8b;

Isoid=000222-2; Sequence=VSP_002032;

Name=C; Synonyms=mGluR8c;

Isoid=000222-3; Sequence=VSP_002034;

-1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

EMBL; U92459; AAB51764.1; --

EMBL; U95025; AAB72040.1; --

EMBL; AJ236921; CAB36968.1; --

EMBL; AJ236922; CAB36969.1; --

HSSP; P23385; LEWT.

Gene; HGNC:4600; GRM8.

MIM; 601116; --

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0008087; P:metabotropic glutamate, GABA-B-like recepto. . .; TAS.

GO; GO:0007194; P:negative regulation of adenylyl cyclase ac. . .; TAS.

GO; GO:0007601; P:visual perception; TAS.

InterPro; IPR001828; ANF receptor.

InterPro; IPR000337; GPCR_Mgr.

DR	InterPro: IPR000162; Mtglu_receptor.	Db	347	SerArgThrLeuAlaAsnAsnArgAsnValTrpPheAlaGluPheTrpGluGluAsn	366
DR	InterPro: IPR000144; Mtglu_receptor8.	QY	124	TTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAGAGGAGGAGCCACATCAAGAGAGTGCACC	183
DR	Pfam: PF01094; ANF_receptor; 1.	Db	367	PheGlyCysLeuLeuGlySerHisGly--LysArgAsnSerHisGlyLeuLeuGlyCysThr	385
DR	PRINTS: PR00248; GPCRMR.	QY	184	AACGAGAGCCATCGGCGCAGACTCGCCCTATGAGCAGAGGAGGAGGAGGAGTGCAGTTCGTG	243
DR	PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.	Db	386	GlyLeuGluArgIleAlaArgAspSerSerTyrGluGlnGluGlyLysValGlnPheVal	405
DR	PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.	QY	244	ATTGACGCTGTGTAGCCATCGGCGCAGCTGCGCAGCGCTGCGCAGCGCTGCGTGTGTC	303
DR	PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.	Db	406	IleAspAlaValTyrSerMetAlaTyrAlaLeuHisAsnMetHisLeuAspLeuGlyCysPro	425
DR	PROSITE: PS00982; G_PROTEIN_RECEP_F3_4; 1.	QY	304	GGCGCGTAGGACTTGCCTCGCATGACCCCGCTGGATGGCAGCCAGCTGCTTAAGTAC	363
KW	Alternative splicing; G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction; Polymorphism; Signal; Transmembrane.	Db	426	GlyTyrIleGlyLeuCysProArgMetSerThrIleAspGlyLysGluLeuGlyTyr	445
FT	SIGNAL 1 33	QY	364	ATCAGGAACGTCAACTTCTCAGGCAATTCGCGGGGAACTGTAACTTCAATGAGAACGGA	423
FT	CHAIN 34 908	Db	446	IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly	465
FT	DOMAIN 34 583	QY	424	GAGCAGCCGGCGCTACGACATCTACCAGTACCACCTGCGCAATGGCTCGSCCCAGTAC	483
FT	TRANSMEM 584 608	Db	466	AspAlaProGlyArgTyrAspIlePheGlnIleThrAsnLysSerThrGluTyr	485
FT	DOMAIN 609 620	QY	484	AAGTCATCGGCTCGTGACAGACACCATGCACTGCAATAGAGCGATGAGTGGCCA	543
FT	TRANSMEM 621 641	Db	486	LysValIleGlyHisTrpThrAsnGlnLeuHisLeuLysValGluAspMetGlnTrpAla	505
FT	DOMAIN 642 647	QY	544	GGGAGTGCCAGAGCTCCCGGCTCCATCTGCGAGTCTGCCCTGCGCAGCCCGGGAGCGA	603
FT	TRANSMEM 648 668	Db	506	HisArgGluHisThrHisProAlaSerValCysSerLeuProCysLeuProGlyGluArg	525
FT	DOMAIN 669 695	QY	604	AAGAGACTGTGAAGGCGATGCTTGTCTGCTGGCACTCGAGCCCTCGCACGGGTACACAG	663
FT	TRANSMEM 696 716	Db	526	LysLysThrValValGlyValProCysSerThrHisCysGluArgCysGluGlyTyrAsn	545
FT	DOMAIN 717 746	QY	664	TACCAAGTGGACCGCTACACCTGTAAGACCTGCCCCCTACGACATGCGCGCCACAGAGAAC	723
FT	TRANSMEM 747 768	Db	546	TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnMetAsn	565
FT	DOMAIN 769 781	QY	724	CGCAGAGCTCCAGCCCATCCCATCTCAAGTTGGAGTGGGACTCGCCGTGGCCGTG	783
FT	TRANSMEM 782 803	Db	566	ArgThrGlyCysGlnLeuIleProIleLeuLeuGluTrpHisSerProTrpAlaVal	585
FT	DOMAIN 804 818	QY	784	CTGCCCTCTTCTGGCGCTGGTGGCATCGCCGCTGCTGCTGGTGGTGGTGGTGGTGGTGGT	843
FT	TRANSMEM 819 843	Db	586	ValProValPheValAlaIleLeuGlyIleIleAlaThrPheValIleValThrPhe	605
FT	DOMAIN 844 908	QY	844	GTGGCTACAAACGATACCCCATCGTCAAGGCTCGGCGCCGCGGAACTGAGCTACGTGCTG	903
FT	CARBOHYD 95 95	Db	606	ValArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeu	625
FT	CARBOHYD 298 298	QY	904	CTGGCGGCGATCTTCTGTGTGTAGCCACTACTTCTCATGATCGCAGAGCCGCGACCTG	963
FT	CARBOHYD 452 452	Db	626	LeuThrGlyIlePheLeuCysTyrSerIleThrPheLeuMetIleAlaAlaProAspThr	645
FT	CARBOHYD 480 480	QY	964	GGGACCTGTTCTCGCTCCGCGCATCTTCTAGGCTCGGCGCTGAGCATGAGCTACGCGGCC	1023
FT	CARBOHYD 565 565	Db	646	IleIleCysSerPheArgArgValPheLeuGlyLeuGlyMetCysPheSerTyrAlaAla	665
FT	VARSPLIC 893 908	QY	1024	CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTAGAGCGGGCAACCGTTCAGT	1083
FT		Db	666	LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysSerValThr	685
FT		QY	1084	GCCCGCGTTCATCAGCCCGCTCGCAGTGGCAGTGGCAGTTCATCTCATCTCTCCCTG	1143
FT		Db	686	AlaProLysPheIleSerProAlaSerGlnLeuValIleThrPheSerLeuIleSerVal	705
FT		QY	1144	CAGTGTCTCGCATCTCGGT	1203
FT		Db	706	GlnLeuLeuGlyValPheValTrpPheValValAspProHisIleIleIleAspTyr	725

Alignment Scores:

Pred. No.:	9,938-134	Length:	908
Score:	2377.00	Matches:	438
Percent Similarity:	85.08%	Conservative:	58
Best Local Similarity:	75.13%	Mismatches:	85
Query Match:	71.96%	Indels:	2
DB:	1	Gaps:	2

US-10-828-332-6 (1-1755) x MGR8_HUMAN (1-908)

QY	7	GGGATATCATCATCTTTGCAAGGAGGATGACA---TCAGGTTGCAACGATCTTCTCC	63
Db	327	GlyAlaValThrIleLeuProLysArgAlaSerIleAspGlyPheAspArgTyrPheArg	346
QY	64	AGCCGACGCTGGACAAACAGGCGCAACATCTCGTGTGCGGATCTCTGGGAGGACAAAC	123

RESULT 9


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Db 646 IleIleCysSerPheArgIlePheLeuGlyLeuGlyMetCysPheSerTyrAlaAla 665
QY 1024 CTGCTGACCAAGCAACCGATTACCGCATCTTTGAGCAGGCAACGCGTGTGAGT 1083
Db 666 LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysLysSerValThr 685
QY 1084 GCCCGCGCTTTTCATCAGCGCCGCTCGCAGCTGCGCATCCTTCATCCTCATCCTCGT 1143
Db 686 AlaProLysPheIleSerProAlaSerGlnLeuValIleThrPheSerLeuIleSerVal 705
QY 1144 CAGCTGCTCGGATCATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1203
Db 706 GlnLeuLeuGlyValPheValThrPheValValAspProProHisThrIleIleAspTyr 725
QY 1204 CAGGACCAACGACACTTACCCCGCTTTCGCGAGGCGGCTCAAGTGGGACACTTCG 1263
Db 726 GlyGluGlnArgThrLeuAspProGlnAsnAlaArgGlyValLeuLysCysAspIleSer 745
QY 1264 GACCTGTCCCTCATCTGCTGCTGGCTACAGCATCTGCTGTGCTGCTGCTGCTGCTG 1323
Db 746 AspLeuSerLeuIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThrVal 765
QY 1324 TAGCGCATCAGACCCGAGGGGTGCGCCGAGACCTTCAACGAGGCGCAACCCCATCGCTTC 1383
Db 766 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 785
QY 1384 ACCATGTACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
Db 786 ThrMetTyrThrThrCysIleIleThrPheLeuAlaPheIleProIlePheGlyThrAla 805
QY 1444 CAGTCAGCGCAGCAAGCTGTACATCCAGACCAACCACTGACGCTGCTGCTGCTGCTG 1503
Db 806 GlnSerAlaGluLysMetTyrIleGlnThrThrThrLeuThrValSerMetSerLeuSer 825
QY 1504 GCTTCAGTGTCCCTGGGATGCTGTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
Db 826 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIlePheHisPro 845
QY 1564 CAGCAGACGTCGCCAGCGCAGCGCAGCTCTCAAGCGCGTGTCCACGCGCCACCATG 1623
Db 846 GluGlnAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThrMet 865
QY 1624 TCCCAAGATTCACACAGAGCGCAACTTCACGCGCCCAATGGGAGGCAACATCAGAGCTG 1683
Db 866 GlnSerLysLeuIleGlnLysGlyAsnAspArgProAsnGlyGluValLysSerGluLeu 885
QY 1684 TGTGAGAACCTGGAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
Db 886 CysGluSerLeuGluThrAsnThrSerSerThrLysThrThrLysSerTyrSerAsp 905
QY 1744 CATGCCATC 1752
Db 906 HisSerIle 908

RESULT 10
MGR7 HUMAN
ID MGR7 HUMAN STANDARD; PRT; 915 AA.
AC Q14831;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Metabotropic glutamate receptor 7 precursor (mGluR7).
GN Name=GRM7; Synonyms=GPRC1G, MGLUR7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96437220; PubMed=8840028;
RA Makoff A., Pilling C., Harrington K., Emson P.;
RT "Human metabotropic glutamate receptor type 7: molecular cloning and
```

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RT mRNA distribution in the CNS.";
RL Brain Res. Mol. Brain Res. 40:165-170(1996).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98141892; PubMed=9473604; DOI=10.1016/S0169-328X(97)00277-5;
RA Wu S., Wright R.A., Rockett P.K., Burgett S.G., Arnold J.S.,
RA Rostek P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
[3]
RP VARIANT PHE-433.
RX MEDLINE=21095249; PubMed=11163549; DOI=10.1016/S0920-9964(99)00235-2;
RA Bolonna A.A., Kerwin R.W., Munro J., Arranz M.J., Makoff A.J.;
RT "Polymorphisms in the genes for mGluR types 7 and 8: association
RT studies with schizophrenia.";
RL Schizophr. Res. 47:99-103(2001).
CC -1- FUNCTION: Receptor for glutamate. The activity of this receptor is
CC mediated by a G-protein that inhibits adenylate cyclase activity.
CC -1- SUBUNIT: Interacts with PRKCAPB (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in many areas of the brain,
CC especially in the cerebral cortex, hippocampus, and cerebellum.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 3 family.
-----
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DR EMBL; X94552; CAA64245.1; -.
DR EMBL; U92458; AAB51763.1; -.
DR HSP; P23385; IEWK.
DR Genew; HGNC:4599; GRM7.
DR MIM; 604101; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . ; TAS.
DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . ; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR00162; Mglu_receptor.
DR InterPro; IPR001883; Mglu_receptor7.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_REC_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_REC_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_REC_F3_3; 1.
DR PROSITE; PS00259; G_PROTEIN_REC_F3_4; 1.
DR G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Polymorphism; Signal; Transmembrane.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 915 Metabotropic glutamate receptor 7.
FT DOMAIN 33 590 Extracellular (Potential).
FT TRANSMEM 591 615 1 (Potential).
FT DOMAIN 616 627 Cytoplasmic (Potential).
FT TRANSMEM 628 648 2 (Potential).
FT DOMAIN 649 654 Extracellular (Potential).
FT TRANSMEM 655 675 3 (Potential).
FT DOMAIN 676 702 Cytoplasmic (Potential).
FT TRANSMEM 703 723 4 (Potential).
FT DOMAIN 724 753 Extracellular (Potential).
FT TRANSMEM 754 775 5 (Potential).
FT DOMAIN 776 788 Cytoplasmic (Potential).
FT TRANSMEM 789 810 6 (Potential).
FT DOMAIN 811 825 Extracellular (Potential).
FT TRANSMEM 826 850 7 (Potential).
FT DOMAIN 851 915 Cytoplasmic (Potential).
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FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 486 486 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).
 FT VARIANT 433 433 Y -> F (in dbSNP:2234977).
 FT /FTID=VAR 003584.
 SQ SEQUENCE 915 AA; 102250 MW; CFF94E06B7F4919 CRC64;

Alignment Scores:

Pred. No.: 2,72e-124 Length: 915
 Score: 2219.00 Matches: 408
 Percent Similarity: 82.53% Conservative: 74
 Best Local Similarity: 69.86% Mismatches: 100
 Query Match: 67.18% Indels: 2
 DB: 1 Gaps: 2

US-10-828-332-6 (1-1755) x MGR7_HUMAN (1-915)

QY 7 GGGGTATCATCATCTTTGGCCACGAGGATGACA---TCAGGGTTCCGACGATCTCTCC 63
 DB 332 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr 351
 QY 64 AGCCGACCTGTCGACAAACAGCGCAACATCTGGTTTGGCCGAGTTCTGGGAGGACAAAC 123
 DB 352 SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluGluAsn 371
 QY 124 TTCATTGCAAGTTGAGCCGCCACCGCTCAAGAGGGAGCCACATCAAGAGTGCACC 183
 DB 372 PheAsnCysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 391
 QY 184 ACCGAGAGCGCATCGGAGGACTCGGCTTATGACGAGGAGGAGTGCAGTTCGTG 243
 DB 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal 411
 QY 244 ATTGACGTGTGTACGCCATGGCCACGCGCTGCACGCCCATGCACCGTCACTGTGTC 303
 DB 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLeuCysAla 431
 QY 304 GGCCGCTAGGACTCTGCTCGCATGGACCCCGTGGATGGACCCAGCTGCTTAAGTAC 363
 DB 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyLysLysLeuLeuLysTyr 451
 QY 364 ATCAGGAAGTCATCTTCAGCATTTGGGGAAACCTGTAACTTCAATGAGAACGGA 423
 DB 452 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471
 QY 424 GAGCACCGGGCGCTACCATCTACCACTGACCACTGCGCAATGGCTCG---GCCGAG 480
 DB 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrSerAsnProGly 491
 QY 481 TACAAGGTTCATCGGCTCGTGGACAGACCACTGCACCTCAGATAGACGCGATGCAGTGG 540
 DB 492 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
 QY 541 CAGGGAGTGGCCAGCAGCTGGCGCTCCATCTGCAGTCTGCTGCTGCCAGCCGCGGGAG 600
 DB 512 GlyLysGlyValArgGluIleProAlaSerValCysThrLeuProCysLysProGlyGln 531
 QY 601 CGAAGAAGCACTGTGAAGGCGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 532 ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr 551
 QY 661 CAGTACCAAGTGGACCGCTACACCTGTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 DB 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
 QY 721 AACCGCAGAGTGGCCAGCCCATTCCTCATAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 780
 DB 572 AsnArgThrGlyCysGlnAspIleProIleIleLysLeuGluTrpHisSerProTrpAla 591
 QY 781 GTGTGCTCCCTTCTCTGCGCGTGGTGGCAGTCCGCGCCAGCTGTTGCTGTGCTGCTGCTGCT 840
 DB 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611

QY 841 TTTGTGCGCTACACGATACCCCATCGTCAAGGCTCGGCGCGGGAAGTACGCTACGTG 900
 DB 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
 QY 901 CTGCTGGCGGGCATCTTTCTGTGTGTACGCCACTACTCTCTCATGATCCAGACGGCGAC 960
 DB 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
 QY 961 CTGGGGACCTGTTCTCGCTCGCGCATCTTCTAGGCGCTGGGATGAGCATCAGTACGG 1020
 DB 652 ValAlaValCysSerPheArgArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
 QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGACGAGGCGAAACGGTGGTC 1080
 DB 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysSerVal 691
 QY 1081 AGTGCCCGCGTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC 1140
 DB 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
 QY 1141 CTGACGCTGCTCGGCATCTGCGTGTGTGGTGGTGGACCCCTCCCATCTCGGTGGAC 1200
 DB 712 ValGlnLeuLeuGlyValPheIleIleTrpPheGlyValAspProProAsnIleIleIleAsp 731
 QY 1201 TTCAGGACCAACGAGACACTTGACCCCGCTTTGGCAGGGCGTGTCTCAAGTGGCATC 1260
 DB 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751
 QY 1261 TCGGACCTGCTCCCTCATCTGCTGGGTGTACGATGCTGCTGATGCTGCTGCTGCTGCT 1320
 DB 752 ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 771
 QY 1321 GTGTACGCGCATCAAGACCGCGGCTGCCGAGACTTCAACGAGCGCAAGCCCATCGCG 1380
 DB 772 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 791
 QY 1381 TTCACATGTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 DB 792 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThr 811
 QY 1441 TCACAGTCAGCGCAGCAAGCTGTACATCCAGACCAACCACTGACCGTCTCCGTGAGTCTG 1500
 DB 812 AlaGlnSerAlaGlyLysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu 831
 QY 1501 AGCGTTCAGTGTCTGCGGATGCTTACATGCTCCCAAGTCTACATCTCTCTTCCAC 1560
 DB 832 SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis 851
 QY 1561 CCGGAGCAGACGTGCCCAAGCGCAGCTCTCAAAGCGGTGTCAACCGCGTCAACCGCGCAC 1620
 DB 852 ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValThrAlaAlaThr 871
 QY 1621 ATGTCCACAAGTTCACACAGAGGCAACTTCAGGCCCAATGGGAGGAGCAAAACAGAG 1680
 DB 872 MetSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 891
 QY 1681 CTGTGTGAGAACCTGAGACCCCGCGTGTGCTACCAACAGACACCTAGCTACCTACAC 1740
 DB 892 LeuCysGluAsnValAspProAsnSerProAlaAlaLysLysLysTyrValSerTyrAsn 911
 QY 1741 AACCATGCCATC 1752
 DB 912 AsnLeuValIle 915

RESULT 11

Q68ED2 PRELIMINARY; PRT; 915 AA.
 ID Q68ED2;
 AC Q68ED2;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Grm7 protein.

GN Name=Gxm7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC080315; AAH80315.1; -;
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Mtblu receptor.
 DR InterPro; IPR001883; Mtblu_receptor7.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR01057; MTABOTROPCTR.
 DR PRINTS; PR00593; MTABOTROPCTR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 SQ SEQUENCE 915 AA, 102218 MW, F0AF7AEDBFBCF71 CRC64;

 Alignment Scores:
 Pred. No.: 5,42e-124 Length: 915
 Score: 2214.00 Matches: 407
 Percent Similarity: 82.53% Conservative: 75
 Best Local Similarity: 69.63% Mismatches: 100
 Query Match: 67.03% Indels: 2
 DB: 2 Gaps: 2

 US-10-828-332-6 (1-1755) x Q68ED2 (1-915)
 QY 7 GGGGTATCATCATCTTTGCCACGAGGATGACA---TCAGGGTTCGACCGGATCTTCCTCC 63
 DB 332 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaIleThrPheThr 351
 QY 64 AGCCCGCAGCTGGACAAACAGCGCCCAACACTCTCGTTTGGCGAGTTCTGGGAGGACAAAC 123
 DB 352 SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTrpTrpGluGluAsn 371
 QY 124 TTCCTTCAGAGTTGAGCGCCGACCGCTTCAGAGAGGAGGAGCCACATCAAGAGTGCAC 183
 DB 372 PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 391

184 AACCGAGAGCGCATCGGGCAGGACTCGCCTATGAGCAGGAGGAGGAGGAGGAGTTCGTG 243
 QY ::
 DB 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal 411
 QY 244 ATTGACGCTGTGTACGCGTGGCGCAGCGCTGACGCCATGACACCGTGTGCTGTGCTCC 303
 DB 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLeuLysCysAla 431
 QY 304 GGCGCGTAGGACTCTCGCCTCGCATGAGACCCCGTGGATGGACCCAGCTGCTTAAGTAC 363
 DB 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyGlyLysLysLeuLeuLysTyr 451
 QY 364 ATCAGGAACGTCACCTCTCAGGATTGCGGGGAACCCCTGTAACTTCAATGACAAACGGA 423
 DB 452 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471
 QY 424 GAGCACCGGGCGCTACGACTTACAGTACCACTGACCACTGCGCAAT---GGTCGCGCGAG 480
 DB 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrThrAsnProGly 491
 QY 481 TACAGGTATCGCTCGTGGACAGACACCTGCACCTCAGATAGAGCGGATGACAGTGG 540
 DB 492 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
 QY 541 CCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCTGCGCTGCCCGCGCGGAG 600
 DB 512 GlyLysGlyValArgGluIleProProSerValCysThrLeuProCysLysProGlyGln 531
 QY 601 CGAAGAAAGCTGTGAAGGGCATGGCTGTGCTGCGCAGCTGCGAGCCCTGACCGGTAC 660
 DB 532 ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr 551
 QY 661 CAGTACCAAGTGGACCGCTACACTGTAAAGACCTGCCCTACGACATGCGGCCACAGAG 720
 DB 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
 QY 721 AACCGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGATGGGAGCTGCCCTGGCGCC 780
 DB 572 AsnArgThrGlyCysGlnAsnIleProIleLysLeuGluTrpHisSerProTyrAla 591
 QY 781 GTGTGCGCTCTTCTGCGCGGTGGGATGCGCCGCGCAGCTGCTGCTGGTGGTGCACG 840
 DB 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611
 QY 841 TTTGTGCGCTACACGATACCCCATCGTCAAGCCCTCGCGCGGAGAACTGAGCTACGTG 900
 DB 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
 QY 901 CTGTGCGCGGCGATCTTCTGTGTGCTAGCCCACTACCTTCTCATGATCGCAGACCGGAC 960
 DB 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
 QY 961 CTGGGAGACTGTTCGCTCCCGCGCATCTTCTAGGGTTCGGCATGAGCATCAGTACGCG 1020
 DB 652 ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
 QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACGGCATCTTTCAGCAGGCGCAACGCTCGGTC 1080
 DB 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal 691
 QY 1081 AGTCCCCCGGCTTTTCATCAGCCCCCGCTCGCAGCTGGCGCATCACCTTTCATCTCTCTCC 1140
 DB 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
 QY 1141 CTGACGTGTCTCGCATCTCGT 1200
 DB 712 ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleIleAsp 731
 QY 1201 TTCAGGACCAACGACACATTGACCCCGCTTTTCAGGCGCGCTCAAGTGCAGACATC 1260
 DB 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751

Qy	64	AGCCGCACGCTGGGACAAACAACAGCGCGCAACATCTGGTTTGCAGAGTCTCGGAGGACCAAC	123
Db	352	SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluGluAsn	371
Qy	124	TTTCATTTGCAGTTGAGCCGCCACCGCTCAAGAAGGGAAGCCACATCAAGAAGTGCACC	163
Db	372	PheAsnCysIysLeuThrIleSerGlySerIysIysGluAspThrAspArgIysCysThr	391
Qy	184	AACCGAGAGCGCATCTCGGCGAGGACTTCGGCCCTATCAGCAGGAGGGAAGTGCAGTTTCGTG	243
Db	392	GlyGlnGluArgIleGlyIysAspSerAsnTyrGlnGlnGluGlyIysValGlnPheVal	411
Qy	244	ATTGACGCTGTGTACGCATGGGCCACGCGCTGCACGCCATGCACCGTGCACCTGTGTGCC	303
Db	412	IleAspAlaValTyrAlaMetAlaHisAlaLeuHisIleMetAsnIysAspLeuCysAla	431
Qy	304	GGCCGCGTAGGACTCTCGCTCGCATGGACCCCGTGGATGGCACCCAGCTGCTTAAGTAC	363
Db	432	AspTyrArgGlyValCysProGluMetGlnAlaGlyGlyIysIysLeuLeuIysTyr	451
Qy	364	ATCAGGAACGTTCAACTTCTCAGGCATTTGCGGGAAACCTCTTAACCTTCAATAGAACCGGA	423
Db	452	IleArgHisValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnIysAsnGly	471
Qy	424	GACGCACCGGGCGCTACGACATCTACAGTACCAGTACCACTGCGCAAT---GGCTCGCGCGAG	480
Db	472	AspAlaProGlyAspTyrAspIlePheGlnTyrGlnThrThrAsnThrThrAsnProGly	491
Qy	481	TACAAGTTCATCGCTCGTGGACAGACACCTGCACCTCAGATAGAGCGGATGCAGTGG	540
Db	492	TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp	511
Qy	541	CCAGGAGTGGCCAGCAGCTCCGCGCTCCATCTGCAGTCTGCCCTCCAGCCCGGGGAG	600
Db	512	GlyIysGlyValArgGluIleProSerSerValCysThrLeuProCysIysProGlyGln	531
Qy	601	CGAAAGAAGACTGTGAAGGGCATGGCTTGCTGGCACTGCGAGCCCTCCACCGGGTAC	660
Db	532	ArgIysIysThrGlnIysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr	551
Qy	661	CAGTACCAAGTGGACCGCTACACTGTAAAGACTGCCCTCAGCATCGCGGCCACACAG	720
Db	552	GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu	571
Qy	721	AACCGCACGAGCTCCACGCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGTGGGCC	780
Db	572	AsnArgThrGlyCysGlnAsnIleProIleIleIysLeuGlnTrpHisSerProTrpAla	591
Qy	781	GTGCTGCCCTCTTCCTCGCGCGTGGTGGCATCGCCGCCACGCTGTTGCTGGTGGTCAAG	840
Db	592	ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr	611
Qy	841	TTTGTGGCTACAAACGATACCCCATCGTCNAGCGCTCGGGCGCGGAACGTAGCTAGCTG	900
Db	612	PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal	631
Qy	901	CTGCTGGCGGCATCTTCTGCTGCACGCCACTACCTCTCTCATGTATCGCAGAGCCGGAC	960
Db	632	LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaIysProAsp	651
Qy	961	CTGGGACCTTCTCGCTCCGCGCATCTCTTAGGGCTCGGCGATGACATCAGCTACGCG	1020
Db	652	ValAlaValCysSerPheArgArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla	671
Qy	1021	GCCCTGTGTACCAAGCAACCGCATTTACCGCATCTTTGACGAGGCGCAACCGTTCGTC	1080
Db	672	AlaLeuLeuThrIysThrAsnArgIleTyrArgIlePheGluGlnGlyIysIysSerVal	691
Qy	1081	AGTGGCCGGTTTCATCAGCCCGCTCCGAGCTGGCGCATCACTTCATCTCATCTCC	1140
Db	692	ThrAlaProArgLeuIleIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer	711
Qy	1141	CTGCAGCTGTCTGGCATCTCGTGTGGTGTGGACCCCTCCCACTCGGTGGTGGAC	1200

[illegible]

DR Pfam: PF00003; 7tm_3; 1.
 DR Pfam: PF01094; ANF_receptor; 1.
 DR Pfam: PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR01057; MTABOTROPICR.
 DR PRINTS; PR00593; MTABOTROPICR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
 DR Receptor.
 SQ SEQUENCE 906 AA; 101301 MW; 53EC7BB83CBB61 CRC64;

Alignment Scores:
 Pred. No.: 1.69e-122 Length: 906
 Score: 2189.00 Matches: 401
 Percent Similarity: 83.39% Conservative: 71
 Best Local Similarity: 70.85% Mismatches: 92
 Query Match: 66.27% Indels: 2
 DB: 2 Gaps: 2

US-10-828-332-6 (1-1755) x Q8NFS2 (1-906)

QY 7 GGGGTATCATCATCTTTCGACAGGAGTACA---TCAGGGTTCGACCGATCTCTCC 63
 DB 332 GlyAlaIleThrIleGlnProlysArgAlaThrValGluGlyPheAspAlaTyrPheThr 351
 QY 64 AGCCGACGCTCGACAAACAGGGCGCAACATCTGTTTGGCGAGTCTTGGGAGGACAAC 123
 DB 352 SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluGluAsn 371
 QY 124 TTCATTTGCAAGTTGAGCGCCGACCGCTCAAGAGGGAGCCACATCAAGAAAGTGCAAC 183
 DB 372 PheAsnCysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 391
 QY 184 AACCCAGAGCGCATCGGCGAGACTCGGCTATGAGCAGGAGGGAGAGTGCAGTTCGTG 243
 DB 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal 411
 QY 244 ATTGACGCTGTAGCCCATGGCCAGCGCTGACCGCTGACCGCATCCACCGTGCCTGCC 303
 DB 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisMetAsnLysAspLeuCysAla 431
 QY 304 GCGCCGCTAGGACTCTGCCCTCGCATGGACCCCGCTGGATGGACCCAGCTGCTTAAGTAC 363
 DB 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyGlyLysLysLeuLeuLysTyr 451
 QY 364 ATCAGAGAGCTCACTTCTCAGGCATTGCGGGGAACCTGTAACTTCAATGAGAACGGA 423
 DB 452 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471
 QY 424 GAGCGACCGGGCGCTACGACATCTACAGTACCACTGCGCAATGGCTCG---GCCGAG 480
 DB 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrAsnThrSerAsnProGly 491
 QY 481 TACAAGGTATCGGCTCGTGGACAGACACCTGCACCTCAGAAATAGAGCGGTAGCAGTGG 540
 DB 492 TyrArgLeuIleGlyGlnTyrPheAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
 QY 541 CCAGGAGTGGCCAGCAGTGGCGCTCCATCTCGTCACTGCTGCTGCGAGCCCGGGAG 600
 DB 512 GlyLysGlyValArgGluIleProAlaSerValCysThrLeuProCysLysProGlyGln 531
 QY 601 CCAAGAGAGACTGTGAAGGCGATGCTGCTGCTGCGACCTGCGAGCCCTGCACCGGGTAC 660
 DB 532 ArgLysLysThrGlnLysGlyThrProCysCysThrTrpThrCysGluProCysAspGlyTyr 551
 QY 661 CAGTACCAAGTGGACCGCTTACACCTGTAAAGACTGCCCCCTACGACATGCGGCCACAGAG 720
 DB 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
 QY 721 AACCCGACAGTGCACGCCCATCCCATCGTCAAGTTGGAGTGGAGTCTGCGCGTGGCC 780

Db 572 AsnArgThrGlyCysGlnAspIleProIleIleLysLeuGluTrpPheHisSerProTrpAla 591
 QY 781 GTGCTGCCCTCTTCTCTGCGCGTGGTGGGCATCGCGGCACGCTGTTGTTGGTGGTCACG 840
 Db 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611
 QY 841 TTTGTCGCTACACGATACCCCATCTCAAGGCTCGGGCGGGAACCTGAGCTACGTCG 900
 Db 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
 QY 901 CTGCTGGCGGCGATCTTCTGTGTACGCCACTACTCTCTCATCATCGACAGCGGAC 960
 Db 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
 QY 961 CTGGGACCTGTCTCGCTCCGCGCATCTTCTAGGCTCGGCATGAGCATCAGTCACGG 1020
 Db 652 ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
 QY 1021 GCCCTGTCAGCAGACCAACCGCATTTACCGCATCTTTGAGCAGGGGCAACGGTCGTC 1080
 Db 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal 691
 QY 1081 AGTGGCCCGCTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC 1140
 Db 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
 QY 1141 CTGACGCTGCTCGGCATCTGCTGTGTGTGGTGGAGCCCTCCCATCTCGTGGTGGAC 1200
 Db 712 ValGlnLeuLeuGlyValPheIleIleTrpPheGlyValAspProAsnIleIleIleAsp 731
 QY 1201 TTCAGGACCAACGGACACTTGACCCCGCTTTGCCAGGGCGTCTCAAGTGGCAGATC 1260
 Db 732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751
 QY 1261 TCGGACCTGCTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGCTGCTGCTGCTACT 1320
 Db 752 ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 771
 QY 1321 GTGTACGCTCAAGACCCGAGCGGTGCGCGAGACTTTCACAGGCGCAAGCCCATCGGC 1380
 Db 772 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 791
 QY 1381 TTCACATGTACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Db 792 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr 811
 QY 1441 TCACAGTCAGCGCACAGCTGTACATCCAGACACACACACACACCTGCTGCTGCTGCTG 1500
 Db 812 AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu 831
 QY 1501 AGCGCTTCAGTGTCTCCGCGGATGCTCTACATGCGCCCAAGTCTACATCATCTCTTCCAC 1560
 Db 832 SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis 851
 QY 1561 CCGGAGCAGAGCTGCCCAAGCGCAGCTCTCAAAGCGGTGGTGCACCGCCGCCAC 1620
 Db 852 ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThr 871
 QY 1621 ATGTCCACACAGTTACACAGAGGGCAACTTCAGGCCCAATGGGAGACCAATACAG 1680
 Db 872 MetSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 891
 QY 1681 CTGTGTGAGAACCTGGAG 1698
 Db 892 LeuCysGluAsnValAsp 897

RESULT 14
 Q8NFS3
 ID Q8NFS3 PRELIMINARY; PRT; 911 AA.
 AC Q8NFS3
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Metabotropic glutamate receptor 7 variant 4.
 GN Name=GRM7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22048149; PubMed=12052533; DOI=10.1016/S0304-3940(02)00306-3;
 RT "Characterization of three novel isoforms of the metabotropic
 glutamate receptor 7 (GRM7).";
 RL Neurosci. Lett. 326:37-40(2002).
 DR EMBL; AF458053; AAM47558.1; -.
 DR HSP; P23385; LEWK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Metglu_receptor.
 DR InterPro; IPR001883; Metglu_receptor7.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCR_MGR.
 DR PRINTS; PR01057; MTABOTROPCTR.
 DR PROSITE; PS00593; MTABOTROPICR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 DR Receptor.
 KW SEQUENCE 911 AA; 101841 MW; 178DC0821EAD05B5 CRC64;

Alignment Scores:

Pred. No.:	1,696-122	Length:	911
Score:	2189.00	Matches:	401
Percent Similarity:	83.39%	Conservative:	71
Best Local Similarity:	70.85%	Mismatches:	92
Query Match:	66.27%	Indels:	2
DB:	2	Gaps:	2

US-10-828-332-6 (1-1755) x QBNFS3 (1-911)

QY	7	GGGGTATCATCATCTTTCCACAGGAGTACAC---TCAGGGTTCGACCGCATCTTCTCC	63
DB	332	GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr	351
QY	64	AGCCGACGCTGGACACACACAGGCGCAACATCTGTTTGGCGAGTTCTGGAGGACAC	123
DB	352	SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluAsn	371
QY	124	TTCCATTGCAAGTTGACGCGCCACCGCTCAAGAGGAGGACCATCAAGAGTGACAC	183
DB	372	PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr	391
QY	184	AACCGAGAGCGCATCGGCGAGACTTCGCCCTATGACGAGGAGGAGGAGGAGTCTG	243
DB	392	GlyGlnGluArgIleGlyLysAspSerAsnTyrGlnGlnGluGlyLysValGlnPheVal	411
QY	244	ATTGACGCTGTGTAGCCATGGCCACCGCTGACCGCATGACCGCTGCTGTCTCC	303
DB	412	IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLysCysAla	431
QY	304	GGCCGCTAGGACTTCGCCCTCGCATGACCGCGGATGGACCGCTGCTTAAGTAC	363
DB	432	AspTyrArgGlyValCysProGluMetGlnAlaGlyGlyLysLysLeuLeuLysTyr	451
QY	364	ATCAGGAACGTCACTTCTCAGGCAATTCGGGGAAACCTGTAACTTCAATGAGAACGGA	423
DB	452	IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly	471

QY	424	GAGCACCGGGCGCTACGACATCTACAGTACCACACTGCGCAATGGCTCG---GCCGAG	480
DB	472	AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrSerAsnProGly	491
QY	481	TACAAGGTTCATCGGCTCGTCGACAGACACCATCTGCACCTCAGAAATAGACGCGATCAGTGG	540
DB	492	TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp	511
QY	541	CCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCTGCCTCCGACCGCGGGAG	600
DB	512	GlyLysGlyValArgGluIleProAlaSerValCysThrLeuProCysLysProGlyGln	531
QY	601	CGAAAGAAAGACTGTGAAGGCGCATGGCTGTCTGCGCAGCTGCGAGCCCTGCACCGGGTAC	660
DB	532	ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr	551
QY	661	CAGTACCAGTGGACCGCTACACTGTAAAGACCTGCCCCCTACGACATGCGCGCCACAGAG	720
DB	552	GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu	571
QY	721	AACGCGACGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGCC	780
DB	572	AsnArgThrGlyCysGlnAspIleProIleLysLeuGlnTrpHisSerProTrpAla	591
QY	781	GTGCTGCCCTCTTCTGCGCGGTGGTGGCATCGCCGACGCTGCTGCTGGTGGTGCACG	840
DB	592	ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr	611
QY	841	TTTGTGCGCTACCAACATACCCCATCGTCAAGCCCTCGGCGCGGAACTAGTACGTG	900
DB	612	PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal	631
QY	901	CTGCTGCGGCGCATCTTCTGCTGCTAGCCCATCTTCTCATGATCGGAGCCGCGAC	960
DB	632	LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp	651
QY	961	CTGGGACCTGTTCTGCTCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTAGCG	1020
DB	652	ValAlaValCysSerPheArgArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla	671
QY	1021	GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAGAGGCGGCAACGTCGCTC	1080
DB	672	AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal	691
QY	1081	AGTCCCGCGGTTTCATCAGCCGCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC	1140
DB	692	ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer	711
QY	1141	CTGACGCTGCTCGGCATCTGCGTGTGGTGTGGTGGACCCCTCCCATCTCGGTGGTGGAC	1200
DB	712	ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleAsp	731
QY	1201	TTCCAGGACCAAGACACATTTGACCCCGCTTTGCCAGGCGGCTGCTCAAGTGGACATC	1260
DB	732	TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle	751
QY	1261	TCGACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1320
DB	752	ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr	771
QY	1321	GTGTACGCCATCAAGACCCGAGGCGTCCGAGACCTTCAACAGAGGCGCAACCCCATCGGC	1380
DB	772	ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly	791
QY	1381	TTACCATGTACACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440
DB	792	PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr	811
QY	1441	TCACAGTACGCGCAGCTGTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1500
DB	812	AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrLeuThrIleSerMetAsnLeu	831

QY 1501 AGCGTTTCAGTTCCTGGGGATGCTTACATGCGCCCAAGTCTACATCATCTCTCCAC 1560
 Db 832 SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis 851
 QY 1561 CGCGAGCAGAACTGTCAGCGCAGCGCAGTCTCAAGCGTGTGTACACCGCGCCACC 1620
 Db 852 ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValThrAlaAlaThr 871
 QY 1621 ATGTCAACAGTTTCACAGAGGCAACTTCAGCGCCCAATGGGGAAGCCAAATCAGAG 1680
 Db 872 MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 891
 QY 1681 CNGTGTGAGAACTGGAG 1698
 Db 892 LeuCysGluAsnValAsp 897

RESULT 15

QNFSA4 PRELIMINARY; PRT; 924 AA.
 AC QNFSA4;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Metabotropic glutamate receptor 7 variant 3.
 GN Name=GRM7;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22048149; PubMed=12052533; DOI=10.1016/S0304-3940(02)00306-3;
 RA Schulz H.L., Stoehr H., Weber B.H.F.;
 RT "Characterization of three novel isoforms of the metabotropic
 RT glutamate receptor 7 (GRM7).";
 RL Neurosci. Lett. 326:37-40(2002).
 DR EMBL; AF458052; AAM47557.1; -;
 DR HSP; F23385; IEWK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000162; Mrglu_receptor.
 DR InterPro; IPR001883; Mrglu_receptor7.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR01057; MTABOTROPIC7.
 DR PRINTS; PR00593; MTABOTROPICR.
 DR PROSITE; PS003979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS003980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS003981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor.
 SQ SEQUENCE 924 AA; 103375 MW; 32028B6156A71BFE CRC64;

Alignment Scores:

Pred. No.: 1.69e-122 Length: 924
 Score: 2189.00 Matches: 401
 Percent Similarity: 83.39% Conservative: 71
 Best Local Similarity: 70.85% Mismatches: 92
 Query Match: 66.27% Indels: 2
 Db: 2 Gaps:

US-10-828-332-6 (1-1755) x QNFSA4 (1-924)

QY 7 GGGGTATCATCATCTTTCACACGAGGATGACA---TCAGGGTTCGACGATCTCTCC 63
 Db 332 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr 351

QY 64 AGCGCAGCTGGACAAACAGCGCGCAACATCTGTTTCCGAGTCTTGGGAGGACAC 123
 Db 352 SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluGluAsn 371
 QY 124 TTCCATTCAAGTTGAGCGCGCCACGCGCTCAAGAGGGAAGCCACATCAAGAAAGTGCACC 183
 Db 372 PheAsnCysLysLeuThrIleSerClySerLysLysGluAspThrAspArgLysCysThr 391
 QY 184 AACGAGAGCGATCGCGCAGCAGCTGCGCCTATAGCAGAGGAGGGAAGGTGAGTTCGTG 243
 Db 392 GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal 411
 QY 244 ATTGACGCTGTAGCGCATCGCGCAGCGCTGACCGCATCGACCGTGCCTGTGTCCTCC 303
 Db 412 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisMetAsnLysAspLeuLysAla 431
 QY 304 GGCGCGTAGACTCTGCTCGCATGGACCCCGTGGATGGCACCAGCTGCTTAAGTAC 363
 Db 432 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyLysLysLeuLeuLysTyr 451
 QY 364 ATCAGGAACGTCAACTTCTCAGGCATTCGCGGGAACCTGTAACTTCAATGAGAACGGA 423
 Db 452 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 471
 QY 424 GACGACCGCGCGCTAGCAGATCTACAGTACCACTGCGCACTGCGCAATGGCTCG---CCCGAG 480
 Db 472 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrSerAsnProGly 491
 QY 481 TACAAGGTTCATCGGCTCGTGACAGACACCTGACACCTCAGAAATAGAGCGGATGAGTGG 540
 Db 492 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 511
 QY 541 CCAGGGAGTGGCCAGCAGCTGCGCGCTCATCTGACGTCTGCTGCTGCGCAGCGCGGGAG 600
 Db 512 GlyLysGlyValArgGluIleProAlaSerValCysThrLeuProCysLysArgProGlyGln 531
 QY 601 CGAAAGAGACTGTGAAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 532 ArgLysLysThrGlnLysGlyThrProCysCysThrTrpCysGluProCysAspGlyTyr 551
 QY 661 CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCGCCCTACGACATCGCGCCACAGAG 720
 Db 552 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 571
 QY 721 AACCGCAGAGCTGCGACCGCATCCCATCATCTCAAGTTGGAGTGGAGTCTGCGCGGGCC 780
 Db 572 AsnArgThrGlyCysGlnAspIleProIleIleLysLeuGluTrpHisSerProTrpAla 591
 QY 781 GTGCTGCGCTCTTCTGCGCGTGGGCGATCGCGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Db 592 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 611
 QY 841 TTTGTGCGCTACACGATACCCCATCGTAAAGCGCTCGCGCGCGGGAACCTGAGTACCTG 900
 Db 612 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 631
 QY 901 CTGCTGCGCGCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Db 632 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 651
 QY 961 CTGGGAGCTTCTGCTGCGCGCATCTTCTAGCGCTGCGGATGAGCATGAGTACGCTACCG 1020
 Db 652 ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 671
 QY 1021 GCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCGGGAACGCGTCCGCTC 1080
 Db 672 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysSerVal 691
 QY 1081 AGTCCCGCGCTTTCATCAGCGCGCTGCGAGCTGGCGCATCACCTTCATCTCATCTCC 1140
 Db 692 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 711
 QY 1141 CTGACGCTGCTCGGCATCTGCGTGGTTCGTGGTGGACCCCTCCCACTCGGTGGTGGAC 1200

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Db      712 ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleAsp 731
Qy      1201 TTCAGGACCAACGGACACTTACCCCGCTTTCAGGCGGCTCAAGTGGACATC 1260
Db      732 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 751
Qy      1261 TCGGACCTGTCCCTCATCTGCTGGCTGCTACAGCATGCTGCTGATGGTCACGTGTACT 1320
Db      752 ThrAspLeuGlnIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 771
Qy      1321 GTGTACGCCATCAAGACCCGAGCGGTGCCCGAGACCTTCAACGAGGCCCAAGCCCATCGGC 1380
Db      772 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 791
Qy      1381 TTCACCATGTACACCACTGATGTCTGGCTGGCTTCATCCCATCTTTTGGACAC 1440
Db      792 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr 811
Qy      1441 TCACAGTCAGCGCAGCAAGCTGTACATCCAGACCAACCACTGACGGTCTCGTGAGTCTG 1500
Db      812 AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrLeuThrIleSerMetAsnLeu 831
Qy      1501 AGCGCTTCAGTGTCCCTGGGATGCTTACATGCCCAAGTCTACATCATCTCTTCCAC 1560
Db      832 SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIlePheHis 851
Qy      1561 CCGGAGCAGACGTGCCCAAGCGCAGCGAGTCTCAAAGCGGTGGTCAACCGCGCCAC 1620
Db      852 ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThr 871
Qy      1621 ATGTCACACAGTTTACACAGAGGGCAACTTCAGGCCCAATGGGAGGCCAAATCAGAG 1680
Db      872 MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 891
Qy      1681 CTGTGTGAGAACCTGGAG 1698
Db      892 LeuCysGluAsnValAsp 897
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Search completed: June 17, 2005, 18:51:06
Job time : 367.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 17, 2005, 18:27:32 ; Search time 67 Seconds
(without alignments)
5040.610 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 3303

Sequence: 1 atgcagggggatcatcatc.....acaccaaccatgccatctag 1755.

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.p/US10828332/runat.17062005.171336.24962/app_query.fasta_1.1927
-DB=PIR -OPWT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODES=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10828332@cgn 1.1.92@runat.17062005.171336.24962 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR.79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3050.5	92.4	912	2 JH0563	metabotropic gluta
2	2336	70.7	908	2 I49142	metabotropic gluta
3	2210	66.9	915	2 A49874	metabotropic gluta
4	2111.5	63.9	551	2 T30806	metabotropic gluta
5	2026.5	61.4	871	2 A46742	metabotropic gluta
6	1171.5	35.5	872	2 JH0561	metabotropic gluta
7	1155.5	35.0	879	2 JCT160	metabotropic gluta
8	1152.5	34.9	879	2 JH0562	metabotropic gluta
9	1123	34.0	1180	2 JCT132	metabotropic gluta
10	1123	34.0	1212	2 JCT131	metabotropic gluta
11	1122	34.0	1199	2 A41939	G protein-coupled
12	1121	33.9	1171	2 A42916	metabotropic gluta
13	1114.5	33.7	1218	2 T71376	glutamate receptor
14	989.5	30.0	999	2 T27628	hypothetical prote

15	871.5	26.4	1267	2 T21340	hypothetical prote
16	691	20.9	1079	2 I59362	calcium/polyvalent
17	683	20.7	1085	2 S40476	Ca(2+)-sensing rec
18	679	20.6	1078	2 A56715	calcium receptor (
19	671	20.3	1088	2 B56715	calcium receptor (
20	308.5	9.3	858	2 JCT683	taste receptor T1R
21	308.5	9.3	1099	2 T16283	hypothetical prote
22	307.5	9.3	1367	1 S48478	glucan 1,4-alpha-g
23	299	9.1	3570	2 T45025	mucin MUC5B, trach
24	281.5	8.5	507	2 T44768	antifreeze glycope
25	278.5	8.4	528	2 I47141	gastric mucin (Clo
26	269.5	8.2	867	2 T45463	membrane glycoprot
27	268	8.1	866	2 T45462	membrane glycoprot
28	259	7.8	797	1 VGBEX1	glycoprotein X pre
29	258.5	7.8	2232	2 T34434	hypothetical prote
30	254	7.7	660	1 QQB33	BHLPI protein - hu
31	250.5	7.6	1032	2 T34433	hypothetical prote
32	245.5	7.4	1952	2 T48814	hypothetical prote
33	241.5	7.3	543	2 S35047	mucin JUL7 - human
34	235	7.1	4776	2 E95206	cell wall surface
35	232.5	7.0	3020	2 A43932	mucin 2 precursor,
36	227.5	6.9	1106	2 JQ0405	hypothetical 119.5
37	218.5	6.6	960	2 JEO356	gamma-aminobutyric
38	216	6.5	1459	2 T32271	hypothetical prote
39	214	6.5	580	2 T43481	probable mucin DXF
40	212.5	6.4	784	2 JQ0317	hypothetical 82k p
41	210.5	6.4	1970	1 S21054	DNA-directed RNA p
42	210.5	6.4	1970	2 I38186	RNA polymerase II
43	209.5	6.3	383	2 T46707	proteophosphoglyca
44	207.5	6.3	610	2 S35049	mucin JER57 - huma
45	207.5	6.3	839	2 T04859	extensin homolog F

ALIGNMENTS

RESULT 1

JH0563 metabotropic glutamate receptor 4 precursor - rat.

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: JH0563; I58149

R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

Neuron 8, 169-179, 1992

A>Title: A family of metabotropic glutamate receptors.

A:Reference number: JH0561; MUID:92110002; PMID:1309649

A:Accession: JH0563

A:Molecule type: mRNA

A:Residues: 1-912 <TAN>

A:Cross-references: UNIPROT:P31423

A:Experimental source: brain

R:O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venesia, D.; McGrane, V.,

Neuron 11, 41-52, 1993

A>Title: The ligand-binding domain in metabotropic glutamate receptors is related to bac

A:Reference number: I58149; MUID:93332699; PMID:8338667

A:Accession: I58149

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-123 'R', 125-912 <RES>

A:Cross-references: GB:M90518; NID:g205400; PIDN:AA93190.1; PID:g205401

C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m

C:Genetics:

A:Gene: GLUR4

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:1-32/Domain: signal sequence #status predicted <SIG>

F:33-912/Product: metabotropic glutamate receptor 4 #status predicted <TRI>

F:588-610/Domain: transmembrane #status predicted <TRI>

F:625-645/Domain: transmembrane #status predicted <III>

F:657-675/Domain: transmembrane #status predicted <III>

F:700-720/Domain: transmembrane #status predicted <IV>

F:751-772/Domain: transmembrane #status predicted <TRV>

F:786-807/Domain: transmembrane #status predicted <TVI>

F:822-847/Domain: transmembrane #status predicted <VII>

F:98,301,454,484,569/Binding site: carboxhydrate (Asn) (covalent) #status predicted
F:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Alignment Scores:

Pred. No.: 6,53e-191 Length: 912
Score: 3050.50 Matches: 575
Percent Similarity: 98.97% Conservative: 2
Best Local Similarity: 98.63% Mismatches: 5
Query Match: 92.36% Indels: 1
DB: 2 Gaps: 1

US-10-828-332-6 (1-1755) x JH0563 (1-912)

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QY 7 GGGGTATCATCTTCCACAGGAGTACA---TCAGGGTTCGACCGATCTTCTCC 63
DB ::::|
330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyPheSer 349
QY 64 AGCCGACGCTGGACAAACAGGCGCAACATCTGGTTTGGCGAGTTCTGGGAGGACAAAC 123
DB ::::|
350 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
QY 124 TTCATTGCAAGTTGAGCGGCACGCGCTCAAGAGGGAAGCCACATCAAGAAGTGCACC 183
DB ::::|
370 PheHisCysLeuSerArgHisAlaLeuLysLysGlySerHisIleLeuLysCysThr 389
QY 184 AACGAGAGCGCTGGCAGACTCTGGCGCTATGACGAGGAGGGAGGTCAGTTCGTG 243
DB ::::|
390 AsnArgGluArgIleGlyGlnAspSerAlaTyrgluGlnGluGlyLysValGlnPheVal 409
QY 244 ATTGACGCTGTGACGCCATGGCCACGCGCTGCACGCGCATGACCGTGACCTGTGTC 303
DB ::::|
410 IleAspAlaValTyrgluMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
QY 304 GCGCGCTGAGACTCTGCGCTCGCATGCAACCGCTGGATGACCCAGCTCTTAAGTAC 363
DB ::::|
430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTy 449
QY 364 ATCAGGACGTCNACTTCTAGGCAATTCGGGGACCTGTAACTTCAATGACGAGA 423
DB ::::|
450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
QY 424 GACGACCGGGCGGTACGACATCTACACAGTACCAACTGCGCAATGGCTCGCGCGAGTAC 483
DB ::::|
470 AspAlaProGlyArgTyrgluIleTyrglnTyrglnLeuArgAsnGlySerAlaGluTy 489
QY 484 AAGTTCATCGCTCTGTGACAGACCACTGCACTCAGAAATAGAGCGGATGAGTGCGCA 543
DB ::::|
490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrpPro 509
QY 544 GGGAGTGGCCAGCAGCTCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCGCGGGAGGA 603
DB ::::|
510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
QY 604 AAGAACTGTGAAGGCGATGCTGTGCTGGCACTCGGACCCCTGACCGCGCTGACCGGTAC 663
DB ::::|
530 LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyrgln 549
QY 664 TACCAAGTGGACCGCTACACCTGTGAAGACCTGCGCTTACGACATGCGCGCCACAGAGAAC 723
DB ::::|
550 TyrGlnValAspArgTyThrCysLysThrCysProTyrgluAspMetArgProThrGluAsn 569
QY 724 GCGCAGAGCTCCAGCCCATCCCATCGTCAAGTTGGAGTGGAGTGGCGCTGCGCGGCGGTG 783
DB ::::|
570 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 589
QY 784 CTGCCCCCTTCTCTGCGCGTGTGGCGATCGCGCGACGCTGCTGCTGGTGGTCTCACGTTT 843
DB ::::|
590 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThrPhe 609
QY 844 GTGCGCTTAAAGATACCCCATCTCAAGGCTCTCGGCGCGGAACTGAGTACGTGCTG 903
DB ::::|
610 ValArgTyrgluAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrgluVal 629
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QY 904 CTGCGCGGCGCTCTTCTGTGTCTACGCGCACTACCTTCTCTCATGTCGAGAGCCGAGACCTG 963
DB ::::|
630 LeuAlaGlyIlePheLeuCysTyrgluThrPheLeuMetIleAlaGluProAspLeu 649
QY 964 GGGACCTGTTCGCTCCGCCGATCTTCTTAGGGCTCGGATAGCATCAGTACGCGGCC 1023
DB ::::|
650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrgluAla 669
QY 1024 CTGCTGACGAGACCAACCACTTACCGCATCTTTCGAGGAGGCAACCGTCCGTCAGT 1083
DB ::::|
670 LeuLeuThrLysThrAsnArgIleTyrgluPheGluGlnGlyLysArgSerValSer 689
QY 1084 GCCCGCGCTTTCATCAGCGCGCTCGCAGCTGGCCATCACCTTCTCATCTCTCCCTG 1143
DB ::::|
690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu 709
QY 1144 CAGTGTCTCGGCTCTCGCTGTGGTTCGCTGGTGAACCCCTCCCACTCGGTGGTGGACTTC 1203
DB ::::|
710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY 1204 CAGGACCAACGCGACCTTGACCCCGCTTTCGCGAGGGCGTCTCAAGTGCACATCTCG 1263
DB ::::|
730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY 1264 GACCTGTCCCTCATCTGCTGGGTACAGCATGCTGTGATGGTCACTGCTGACTGTG 1323
DB ::::|
750 AspLeuSerLeuIleCysLeuLeuGlyTyrgluSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TAGCCCATCAAGACCCGAGCGTGCAGACCTTCAACGAGGCGCAAGCCCATCGGCTTC 1383
DB ::::|
770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACCATGTACACCACTGCATGTGTGCTGGCTTCATCCCATCTTTTGGCACCTCA 1443
DB ::::|
790 ThrMetTyrgluThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
QY 1444 CAGTACGCGCACAGCTGTATCATCCAGAACACACACTGACGGTCTCCGTGAGTCTCAGC 1503
DB ::::|
810 GlnSerAlaAspLysLeuTyrgluIleGlnThrThrLeuThrValSerValSerLeuSer 829
QY 1504 GCTTCAGTGTCCCTGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
DB ::::|
830 AlaSerValSerLeuGlyMetLeuTyrgluMetProLysValTyrgluIleLeuPheHisPro 849
QY 1564 GAGCAGACGCTGCCAGCGCAGCGCAGCTCAAAAGCGTGTCCAGCGCGCCACCATG 1623
DB ::::|
850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
QY 1624 TCCAACTGTTTACACAGAGGCGCACTTCAGGCGCCCAATGGGAGGCAATCAGAGCTG 1683
DB ::::|
870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACCTGGAGACCCGAGCGCTGCTACCAACAGACCTACGTACCTACACCAAC 1743
DB ::::|
890 CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrgluValThrTyrgluAsn 909
QY 1744 CATGCCATC 1752
DB ::::|
910 HisAlaIle 912
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RESULT 2

149142

metabotropic glutamate receptor 8 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: 149142

R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.

J. Neurosci. 15, 3075-3083, 1995

A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory

A:Reference number: 149142; PMID:7722646

A:Accession: 149142

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-908 <RES>
A;Cross-references: UNIPROT:P47743; EMBL:U17252; NID:G854728; PIDN:AAA68149.1; PID:G854728
C;Genetics:
A;Gene: mGluR8
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: neurotransmitter receptor

Alignment Scores:		
Pred. No.:	2,18e-144	908
Score:	2336.00	432
Percent Similarity:	84.39%	Conservative: 89
Best Local Similarity:	74.10%	Mismatches: 89
Query Match:	70.72%	Indels: 2
DB:	2	Gaps: 2

US-10-828-332-6 (1-1755) x I49142 (1-908)

Qy	7	GGGGTATCATCATCTTTGGCAACGAGGATGACA---TCAGGTTTGACCGATCTTCTCC	63
Db	327	GlyAlaValThrIleLeuProLysArgAlaSerIleAspGlyPheAspArgTyrPheArg	346
Qy	64	AGCGCAGCTGGACACAACAAGCGCAACATCTGTTTGGCAGTTCGGGAGGACAAC	123
Db	347	SerArgThrLeuAlaAsnArgArgAsnValTrpPheAlaGluPheSerGluGlyAsn	366
Qy	124	TTCCATTGCAAGTTGAGCGCCACCGCTCAAGAAGGGAAGCCACATCAAGAAGTGCACC	183
Db	367	PheGlyCysLysSerGlySerHisGly--LysArgAsnSerHisIleLysLysCysThr	385
Qy	184	AACGAGAGCGCATCGGCAGGACTCGGCCTATAGCAGGAGGGAGGTGCAGTTCGTG	243
Db	386	GlyLeuGluArgIleAlaArgAspSerTyrGluGlnGluGlyLysValGlnPheVal	405
Qy	244	ATTGACGCTGTGACGTCATGGCCACGCGCTGCAGCCATGCACCGTCACCTGTCTGCC	303
Db	406	IleAspAlaValTyrSerMetAlaTyrAlaLeuHisAsnMetHisLysGluLeuCysPro	425
Qy	304	GGCGCGTGGACTCTGCCCTCGCATGAGACCCCGTGGATGGCACCCAGCTGTTAAGTAC	363
Db	426	GlyTyrIleGlyLeuCysProArgMetValThrIleAspGlyLysGluLeuLeuGlyTyr	445
Qy	364	ATCAGGAACGTCACCTCTCAGGCATTCGGGGACCCCTGTAACTTCAATCAGACCGA	423
Db	446	IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly	465
Qy	424	GACGACCGGGCGGTACGACATCTACCAAGTACCAACTCGCGCAATGGCTCGCGCCGAGTAC	483
Db	466	AspAlaProGlyArgTyrAspIlePheGlnTyrGlnIleAsnAsnLysSerThrGluTyr	485
Qy	484	AAGTTCATCGGCTCGTGACAGACACCTGCGACCTCAGCATAGAGCGGATGAGTGGCCA	543
Db	486	LysIleIleGlyHisIleTrpThrAsnGlnLeuHisLeuLysValGluAspMetGlnTrpAla	505
Qy	544	GGGAGTGGCCAGCAGCTCGCGGCTCCATCTCAGTCTGCCCTGCGCAGCCCGGGAGCCA	603
Db	506	AsnArgGluHisThrHisProAlaSerValCysSerLeuProCysIleProGlyGluArg	525
Qy	604	AAGAAGACTGTGAAGGGCATGGCTTGTCTGGCAGTTCGAGCCCTGCGACCGGTACCAAG	663
Db	526	LysLysThrValLysGlyValProCysCysIleHisCysGlyArgCysGluGlyTyrAsn	545
Qy	664	TACCAAGTGGACCGCTACACCTGTAAGACCTGCCCTACGACATGGCGGCCACAGAGAC	723
Db	546	TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnIleAsn	565
Qy	724	CGCACGAGCTGCCGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGCTGGCGCGG	783
Db	566	ArgThrGlyCysGlnArgIleProIleIleLysLeuGluTrpHisSerProIleAlaVal	585
Qy	784	CTGCCCTCTCTCGGCGGTGGGCAATCGCCCGCCACGCTGTTGTGTGTGTACGTTT	843
Db	586	ValProValLeuIleAlaIleLeuGlyIleIleAlaThrThrPheValIleValThrPhe	605

RESULT 3

A49874
metabotropic glutamate receptor 7 - rat
N;Alternate names: metabotropic glutamate receptor mGluR7
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_0
C;Accession: A49874.1 I57954
R;Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemura, R.; Biol. Chem. 269, 1231-1236, 1994

A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coup
A:Reference number: A49874; MUID:94117433; PMID:8288585
A:Accession: A49874
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
A:CROSS-references: UNIPROT:P35400; GB:D16817; NID:g458728; PIDN:BA04092.1; PID:g458729
R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.
Mol. Pharmacol. 45: 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid
A:Reference number: I57954; MUID:94195260; PMID:8145723
A:Accession: I57954
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
A:CROSS-references: EMBL:U06832; NID:g459657; PIDN:AAA20655.1; PID:g459658
C:Genetics:
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor

Alignment Scores:
Pred. No.: 3,496-136 Length: 915
Score: 2210.00 Matches: 406
Percent Similarity: 82.53% Conservative: 76
Best Local Similarity: 69.52% Mismatches: 100
Query Match: 66.91% Indels: 2
DB: 2 Gaps: 2

US-10-828-332-6 (1-1755) x A49874 (1-915)

QY	7	GGGGTATCATCATCTTCCACGAGGATGACA---TCAGGGTTCGACCGATACTTCTCC	63
DB	332	GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAsnAlaTyrPheThr	351
QY	64	AGCCGACGCTGGACAAACACAGGCGCAACATCTGGTTTGGCGAGTTCTGGGAGACAAAC	123
DB	352	SerArgThrLeuGluAsnAsnArgAsnValTrpPheAlaGluTyrTrpGluAsn	371
QY	124	TTCCATTGCAAGTTGAGCGCCACCGCTCAAGAGGAGGACCATCAAGAAGTGACCC	183
DB	372	PheAsnCysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr	391
QY	184	AACCGAGAGCGCATCGCGCAGGACTCGCCCTATGAGAGGAGGAGGAGTGCAGTCTGTG	243
DB	392	GlyGlnGluArgIleGlyAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal	411
QY	244	ATTGACGCTGTGTACGCCATGGCCACCGCTGCACCGCCATGCCACCTGTGTCCC	303
DB	412	IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLeuCysAla	431
QY	304	GGCCCGGTAGGACTGTGCTCGCATGGACCCCGTGGATGGACCCAGCTGCTTAAGTAC	363
DB	432	AspTyrArgGlyValCysProGluMetGluGlnAlaGlyLysLysLeuLeuLysTyr	451
QY	364	ATCAGGACGTCACCTCTCAGGCATTGCGGGACCTGTAACTTCAATGAGAACGGA	423
DB	452	IleArgHisValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly	471
QY	424	GACGACCGGGCGGTACGACATCTACAGTACCAACTCGCGCAAT---GGCTCGGCGGAG	480
DB	472	AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrAsnThrThrAsnProGly	491
QY	481	TACAAGGTCTCGGCTGTGGACAGACCATCTGCACCTCAGAAATAGACGGATGACATGG	540
DB	492	TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp	511
QY	541	CCAGGAGTGGCGACGCTCGCGCTCCATCTCAGTCTGCTGCTGCTGCTGCTGCTGCTG	600
DB	512	GlyLysGlyValArgGluIleProSerValCysThrLeuProCysLysProGlyGln	531
QY	601	CGAAAGAGACTGTGAAGGGCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660

DB	532	ArgLysLysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr	551
QY	661	CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCCCTACGACATGCGGCCACAGAG	720
DB	552	GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu	571
QY	721	AACCGCAGAGCTGCCAGCCCATCCCCCATCGTCAAGTTGGAGTGGGACTCGCGTGGGCC	780
DB	572	AsnArgThrGlyCysGlnAsnIleProIleIleLysLeuGluTrpHisSerProTyrAla	591
QY	781	GTGTCGCCCTCTTCTTCTGGCGGTGGGATGCCCGCCAGCTGTTGTTGTTGTTGTTGTTG	840
DB	592	ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr	611
QY	841	TTTGTGGCTACACGATACCCCATCGTCAAGSCCTCGGCGGGGAACCTAGCTACGTG	900
DB	612	PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal	631
QY	901	CTGCTGGCGGCATCTTTCTGTGTACGCCACTACCTTCTCTCATGATCGCAGACCCGAC	960
DB	632	LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp	651
QY	961	CTGGGAGCTTGTCTCGCTCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTACGC	1020
DB	652	ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla	671
QY	1021	GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGCAACGCGTCCGTC	1080
DB	672	AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal	691
QY	1081	AGTCCCCCGGCTTTTCATCAGCCCGGCTCGCAGCTGGCCATCACCTTCTCATCTCTCC	1140
DB	692	ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer	711
QY	1141	CTGAGCTGTCTCGCATCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1200
DB	712	ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProAsnIleIleIleAsp	731
QY	1201	TTCCAGGACCAACGACACTTGACCCCGCTTTTCCAGGGCGGTCTCAAGTCGACATC	1260
DB	732	TyrAspGluHisLysThrMetAsnProGluAlaArgGlyValLeuLysCysAspIle	751
QY	1261	TCGACCTGTCTCTCATCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1320
DB	752	ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr	771
QY	1321	GTGTACGCCATCAAGACCCGAGGGTCCCGAGACCTTCAACGAGGCGCAACCCATCGGC	1380
DB	772	ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly	791
QY	1381	TTACCATGTACACCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1440
DB	792	PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr	811
QY	1441	TCACAGTCAGCCGACAAAGCTGTATCATCCAGAACACACACTGACGGTCTCGGTGCTGT	1500
DB	812	AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu	831
QY	1501	AGCGCTTCAGTGTCCCTGGGATGCTCTACATGCCCAAGTCTACATCATCTCTCTCCAC	1560
DB	832	SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis	851
QY	1561	CCGAGCAGACGTCGCCCAAGCGACGAGTCTCAAGCGCGGTGCACCGCCGCCACCC	1620
DB	852	ProGluLeuAsnValGlnLysArgLysSerPheLysAlaValThrThrAlaAlaThr	871
QY	1621	ATGTCCAAACAGTTTACACAGAGGCAACTTTCAGGCCCAATGGGGAAGCCAAATCAGAG	1680
DB	872	MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu	891
QY	1681	CTGTGTGAGAACCTGGAGACCCCGCGCTGGCTACCAACAGACCTAGCTCAGCTACACC	1740
DB	892	LeuCysGluAsnValAspProAsnSerProAlaAlaLysLysTyrValSerTyrAsn	911

QY 1741 AACCATGCCATC 1752
DB 912 AsnLeuValille 915

RESULT 4
T30806
metabotropic glutamate receptor 7 - Fugu rubripes (fragment)
C:Species: Fugu rubripes
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T30806
R: Cottage, A.J.; Clark, M.; Hawker, K.; Umrana, Y.; Wheller, D.; Bishop, M.; Elgar, G.
PDBS Lett. 443, 370-374, 1999
A:Title: Three receptor genes for plasminogen related growth factors in the genome of th
A:Reference number: Z20880; MUID:99148833; PMID:10025966
A:Accession: T30806
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-551 <COT>
A:Cross-references: UNIPROT:Q9PWQ0; EMBL-AJ010317; NID:e1355235; PID:e1355236; PIDN:CAAC
C:Genetics:
A:Gene: GRM7
A:Note: intron positions not resolved (incomplete sequence)
C:Superfamily: metabotropic glutamate receptor 4

Alignment Scores:
Pred. No.: 8,79e-130 Length: 551
Score: 2111.50 Matches: 376
Percent Similarity: 83.88% Conservative: 82
Best Local Similarity: 68.86% Mismatches: 87
Query Match: 63.93% Indels: 1
DB: 2 Gaps: 1

US-10-828-332-6 (1-1755) x T30806 (1-551)

QY 46 TTCGACCGATCTTCTCCAGCCGACGCTGGACAAACAGCGCAACATCTGGTTGCC 105
DB 1 PheAspGlnTyrPheThrSerArgSerLeuGluAsnAsnArgAArgenilleTrpPheala 20
QY 106 GAGTTCTGGGAGGACAACTTCCATTGCAATTGAGCGCGCCACGCGCTCAAGAGGGAAAGC 165
DB 21 GluPheTrpGluAspAspPheLysLysLeuThrArgProGlyIleLysLeuThrGluLeu 40
QY 166 CACATCAAGAAGTCACCAACCCAGAGAGCGATCGGCGAGACTCGGCTATGACGAGAG 225
DB 41 GlyArgGlyLysThrGlyAspGluArgLysSerArgAspSerGlnTyrGluGlnGlu 60
QY 226 GGGAAAGGTGCAGTTCGTGATTGACGCTGTGTAGCGCCATGGGCCACGCGCTCGACGCCATG 285
DB 61 GlyLysValGlnPheValilleAspAlaValTyrAlaMetAlaHisAlaLeuHisSerMet 80
QY 286 CACCGTGACCTGTGTCGGCCGCGTAGGACTCTGCGCTCGCATGGAGACCCCGTGGATGGC 345
DB 81 HisThrAspLeuCyseProGlySerMetGlyValCyseAspLysMetAspProValGluGly 100
QY 346 ACCCAGCTGCTTAAGTACATCAGGAACGTCACTTCTCAGSCATTGCGGGGAACCCCTGTA 405
DB 101 ArgMetLeuLeuGlnTyrIleHisGlyValAsnPheAsnGlySerAlaGlyThrGlyVal 120
QY 406 ACCTTCAATGAGACGAGACGACCGGGGCGCTACGACATCTACCAAGTACCAACTGCGC 465
DB 121 MetPheAsnGluAsnGlyAspAlaProGlyArgTyrAspIlePheGlnTyrGlnMetSer 140
QY 466 AAT---GGCTCGGCGAGTACAAGGTATCTCGGCTCTGGAGACAGACCACTGCACCTCAGA 522
DB 141 AsnIleSerAsnProGlyTyrArgAsnIleGlyGlnTrpThrAsnHisLeuArgLeuAsn 160
QY 523 ATAGAGCGGATGAGTGGCGGAGGAGTGGCGAGCTGCGCGCTCCATCTGAGTCTG 582
DB 161 LeuGluGluMetGlnTrpSerGlyGlyAspArgLysIleProGluSerValCyseSerPhe 180
QY 583 CCCTGCCAGCCCGGAGGAGCAAGAGACTGTGAAGGGCATGCTTCTGCTGCACATGCG 642

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RESULT 5
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46742
R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, J.
J. Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor mGluR6
A:Reference number: A46742; MUID:93280152; PMID:8389366
A:Accession: A46742
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NA>
A:Cross-references: UNIPROT:P35349; GB:D13963; NID:g391856; PIDN:BA03066.1; PID:g391857
A:Experimental source: retina
A>Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:P:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein

Alignment Scores:
Pred. No.: 3 096-124 Length: 871
Score: 2026.50 Matches: 379
Percent Similarity: 74.24% Conservative: 62
Best Local Similarity: 63.80% Mismatches: 97
Query Match: 61.35% Indels: 56
DB: 2 Gaps: 2

US-10-828-332-6 (1-1755) x A46742 (1-871)
QY 3 GCCAGGGTATCATCTTTGCCAAGCAGGATGACATCA----- 42
DB 267 AlaArgGlyIleIleIlePheAlaAsnGluAspAep-IleArgValLeuGluAlaTh 286
QY 42 ----- 42
DB 286 rArgGlnAlaAsnLeuThrGlyHisPheLeuTrpValGlySerAspSerTrpGlySerLy 306
QY 42 ----- 42
DB 306 sIleSerProIleLeuAsnLeuGluGluAlaValGlyAlaIleThrIleLeuProLy 326
QY 43 -----GGTTCGACCGATCTTCTCCAGCGCAGCGCGGACACACAG 86
DB 326 sArgAlaSerIleAspGlyPheAspGlnTrpPheMetThrArgSerLeuGluAsnAsnAr 346
QY 87 CGCAACATCTGTTTGGCGAGTCTGGGAGGACAACTTCCATTGCCAAGTTGAGCGCGCA 146
DB 346 gArgAsnIleTrpPheAlaGluPheTrpGluAsnPheAsnCyAsyLeuThrSerSe 366
QY 147 CGCGCTCAAGAGGAGCCATCAAGATGACCAACCGAGAGCGATCGGGCAGGA 206
DB 366 rGlyGlyGlnSerAspAspSerThrArgLysCysThrGlyGluGluArgIleGlyGlnAs 386
QY 207 CTCGGCTATGACGAGGAGGAGGAGTCTGATTCGATTCAGCTGTGTACGCGATGG 266
DB 386 pSerAlaTrpGluGlnGluGlyLysValGlnPheValIleAspAlaValIleAlaIleAl 406
QY 267 CCACCGCTGACGCGCATCGCGTACCTGTGTCCCGCGCGGTAGGACTCTGCGCTCG 326
DB 406 aHisAlaLeuHisSerMetHisGlnAlaLeuCysProGlyHisThrGlyLeuCyProAl 426
QY 327 CATGACCCCGTGGATGGACCCAGCTGTTAAGTACATCAGGAACGCTCACTCTCAGG 386
DB 426 aMetGluProThrAspGlyArgThrLeuLeuHisTyrIleArgAlaValArgPheAsnGl 446
QY 387 CATTCGGGGGACCTGTAACTTCAATCAGAACGAGACCGACCGGGCGCTACGACAT 446
DB 446 ySerAlaGlyThrProValMetPheAsnGluAsnGlyAspAlaProGlyArgTyrAspIl 466
QY 447 CTACAGGTACCAACTCGCGCAATGGCTCGGCGGAG-----TACAAGGTGTCATCGGCTC 497
DB 497 ----- 497
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DB ePheGlnTrpGlnAlaThrAsnGlySerAlaSerSerGlyGlyTrpGlnAlaValGlyGl 486
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DB nTrpAlaGluAlaLeuArgLeuAspMetGluValLeuArgTrpSerGlyAspProHisGl 506
QY GCTGCGCGCTGCCATCTGCAGTCTGCCCTCCAGCCCGGGGAGCGAAAGAGACTGTGAA 617
DB uValProProSerGlnCysSerLeuProCyAsyGlyProGlyGluArgLysMetValLy 526
QY GGGCATCGTGTCTGTGGCAGTCTGCAGCCCTGCACCGGGTACCATGACAGTGGACCG 677
DB sGlyValProCysCyStrPHisCySgIuAlaCyAspGlyTyrArgPheGlnValAspGl 546
QY CTACACCTGTAAAGACCTGCCCTACGACATGCGGCCCCACAGAGAACCGACGCTGCCA 737
DB uPheThrCySgIuAlaCySProGlyAspMetArgProThrProAsnHisThrGlyCyAsr 566
QY GCCCATCCCATCTCAAGTTGGAGTGGGACTCGCCCGTGGCGCGTGTGCCCCCTCTTCT 797
DB gProThrProValValArgLeuThrTrpSerSerProTrpAlaAlaLeuProLeuLeu 586
QY GCGCGTGTGGGATCGCCGCGCAGCTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 857
DB uAlaValLeuGlyIleMetAlaThrThrIleMetAlaThrPheMetArgHisAsnAs 606
QY TACCCCATCGTCAAGGCGCTCGGCGCGGAACTGAGCTAGCTGTGTGTGTGTGTGTGTGT 917
DB pThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeuLeuThrGlyIlePh 626
QY TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 977
DB eLeuIleTrpAlaIleThrPheLeuMetValAlaGluProCySAlaIleCySAlaAl 646
QY CCGCGCATCTTCTCAGGCTCGGCGCATGAGCATCAGTACGCGGCGCTGTGTGTGTGTGT 1037
DB aArgArgLeuLeuLeuGlyLeuGlyThrThrLeuSerTyrSerAlaLeuLeuThrLyTh 666
QY CACCGCATTTTACCGCATCTTGTGAGCGGCGCAACGCTCGGTGAGTGTGTGTGTGTGTGT 1097
DB rAsnArgIleTrpArgIlePheGluGlnGlyLysArgSerValThrProProPheIl 686
QY CAGCGCGCTCGCAGCTGCGCATCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1157
DB eSerProThrSerGlnLeuValIleThrPheGlyLeuThrSerLeuGlnValValGlyVa 706
QY CTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1217
DB lIleAlaTrpLeuGlyAlaGlnProProHisSerValIleAspTyrGluGlnArgTh 726
QY ACTTGACCCCGCTTTCAGGCGCGTGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1277
DB rValAspProGluGlnAlaArgGlyValLeuLysCyAspMetSerAspLeuSerLeuIl 746
QY CTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1337
DB eGlyCySLeuGlyTyrSerLeuLeuLeuMetValThrCysThrValIleAlaIleLysAl 766
QY CCGAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1397
DB aArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPheThrMetTyrThrTh 786
QY CTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1457
DB rCySileIleTrpLeuAlaPheValProIlePhePheGlyThrAlaGlnSerAlaGluLy 806
QY GCTGTATATCCAGAACCAACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1517
DB sIleTyrIleGlnThrThrThrLeuThrValSerLeuSerLeuSerAlaSerValSerLe 826
QY GGGATGCTGTATGCGCCAAAGTCTCATCATCTCTCTTCCACCGGAGCAGACGTGCC 1577
DB uGlyWetLeuTrpValProLyStrThrThrValIleLeuPheHisProGluGlnAsnValGl 846
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QY 1578 CAAAGCCGACGAGTCTCAAGCCGTGTCTACCGCCGCC 1617
 Db 846 nlysaArgysaSerLeuylsYthrSerThrMetAla 859

RESULT 6
 JH0561
 metabotropic glutamate receptor 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JH0561
 R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 Neuron 8, 169-179, 1992
 A:Title: A family of metabotropic glutamate receptors.
 A:Reference number: JH0561; MUID:92110002; PMID:1309649
 A:Accession: JH0561
 A:Molecule type: mRNA
 A:Residues: 1-872 <TAN>
 A:Cross-references: UNIPROT:P31421
 A:Experimental source: brain
 C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m
 C:Superfamily: metabotropic glutamate receptor 4
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
 F:568-590/Domain: transmembrane #status predicted <TRI>
 F:605-625/Domain: transmembrane #status predicted <TRI>
 F:637-655/Domain: transmembrane #status predicted <TRI>
 F:680-700/Domain: transmembrane #status predicted <TRI>
 F:726-747/Domain: transmembrane #status predicted <TRI>
 F:761-782/Domain: transmembrane #status predicted <TRI>
 F:795-819/Domain: transmembrane #status predicted <VII>
 F:203,286,338,402,547/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:601,675,827,843/Binding site: phosphate (Ser) (covalent) #status predicted
 F:832/Binding site: phosphate (Thr) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 1,45e-68 Length: 872
 Score: 1171.50 Matches: 249
 Percent Similarity: 57.65% Conservative: 75
 Best Local Similarity: 44.31% Mismatches: 197
 Query Match: 35.47% Indels: 41
 DB: 2 Gaps: 10

US-10-828-332-6 (1-1755) x JH0561 (1-872)

QY 10 GTATCATCTTCCACGAGGATGACATCAGGGTTCGACCGATCTCTCCAGCCG 69
 Db 11eThrIleGluLeuAlaSerTyrProIleSerAppPheAlaSerTyrPheGlnSerLeu 334
 QY 70 ACGCTGGACAAACAGCGCGCAACATCTGTTTTCGAGTCTCGGAGGACAACTTCCAT 129
 Db 335 AppProTpaAsnAsnSerArgAsnProTyrPheArgGluPheTyrGluArgPheHis 354
 QY 130 TCAAGTTG-----ACCGCCACGCGCTCAAGAGGAGGAGCCACATCAAG 174
 Db 355 CysSerPheArgGlnArgAspCysAlaAlaHisSerLeuArgAla----- 369
 QY 175 AAGTCACCCAGGAGCGCATCGGCGAGGACTCGGCTATGACGAGGAGGAGGTG 234
 Db 370 -----ValProPheGluGlnGluSerLysIle 378
 QY 235 CAGTTTCGTATTGACGTGTACGCCATGGCGCGCTCCAGCCATGACCGGTGAC 294
 Db 379 MetPheValValAsnAlaValTyrAlaMetAlaHisAlaLeuHisAsnMethHisArgAla 398
 QY 295 GTGTGTCCCGCGCGTAGACTCTGCTCGCATGAGCCCGCGTGGATGGCCACCGCTG 354
 Db 399 LeuCysProAsnThrThrHisLeuCysAspAlaMetArgProValAsnGlyArgLeu 418
 QY 355 CTTAG-----TACATCAGGAGCTCACTTCTCA-----GGCATTCGGGG 396
 Db 419 TyrLysAspPheValLeuAsnValLysPheAspAlaProPheArgProAlaAspThrAsp 438

QY 397 AACCTCTGTAACCTTCAATGAGAACGAGACGACCGCGGCGCTACGACATCTACCGATAC 456
 Db 439 AspGluValArgPheAspArgPheGlyAspGlyIleGlyArgTyrAsnIlePheThrTyr 458
 QY 457 CAACTGCGCAATGGCTCGCGCGAGTACAGGTC-----ATCGGCTCGTGAGACAGACCAC 510
 Db 459 ---LeuArgAlaGlySerGlyArgTyrGlnLysValGlyTyrTrpAlaGluGly 477
 QY 511 CTGACCTCTCAGAAATAGAGCGATGAGTGG-----CCAGGAGGAGCGGAGCGAGTGGCG 564
 Db 478 LeuThrLeuAspThrSerPheIleProTyrPalaSerProSerAlaGly---ProLeuPro 496
 QY 565 CCTCTCATCTGACAGTCTCCCTGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 624
 Db 497 AlaSerArgCysSerGluProCysLeuGlnAsnGluValLysSerValGlnProGlyGlu 516
 QY 625 GCTTGCTGCTGCGACTGCGCGCGCGTACCGCGGTACCAAGTACCAAGTACCGCGTACACC 684
 Db 517 ValCysCysTrpLeuCysIleProCysGlnProTyrGluTyrArgLeuAspGluPheThr 536
 QY 685 TGTAAAGACTGCGCCCTACGACATGCGCGCGCGCACAGAGAACCGCAGAGTGGCGGCGCATC 744
 Db 537 CysAlaAspCysGlyLeuGlyTyrTrpProAsnAlaSerLeuThrGlyCysPheGluLeu 556
 QY 745 CCCATCGTCAAGTTGGAGTGGAGTCTCGCGCGCGTGGCGTGGTGGTGGTGGTGGTGGTGG 804
 Db 557 ProGlnGluTyrIleArgTyrGlyAspAlaTrpAlaValGlyProValThrIleAlaCys 576
 QY 805 GTGGGATCGCGCGCGCGCGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 864
 Db 577 LeuGlyAlaLeuAlaThrLeuPheValLeuGlyValPheValArgHisAlaThrPro 596
 QY 865 ATCTGCAAGGCTCGGCGCGCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 924
 Db 597 ValValLysAlaSerGlyArgGluLeuGlyCysTyrIleLeuLeuGlyValPheLeuCys 616
 QY 925 TACGCCACTACTTCTCTCATGATCGACGCGGAGCTGGGAGCTGGTGGTGGTGGTGGTGGTGG 984
 Db 617 TyrCysMetThrPheValPheIleAlaLysProSerThrAlaValCysThrLeuArgArg 636
 QY 985 ATCTCTCTAGGCTCGGCGCGCGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1044
 Db 637 LeuGlyLeuGlyThrAlaPheSerValCysTyrSerAlaLeuLeuThrLysThrAsnArg 656
 QY 1045 ATTTACCCGATCTTTGAGCAGCGGCAACGCTCGGTCAGTGGCGCTGGTGGTGGTGGTGGTGG 1104
 Db 657 IleAlaArgIlePheGlyAlaArgGluGlyAlaGlnArgProArgPheIleSerPro 676
 QY 1105 GCCTGCGAGCTGGCGCATCACCTTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1164
 Db 677 AlaSerGlnValAlaIleCysLeuAlaLeuIleSerGlyGlnLeuLeuIleValAlaAla 696
 QY 1165 TGGTTCGTGGTGGAGCCCTCCATCGGTGGTGGAGCTTCCAGGACCAAGGAGCAGTTCGAC 1224
 Db 697 TrpLeuValValGluAlaProGlyThr-----GlyLysGluThrAlaPro 711
 QY 1225 CCGCGTTTGGCGGCGGTCTCAAGTGCAGATCTCGGACCTCTCCCTCTCTCTCTCTCTCTCTCT 1284
 Db 712 GluArgArgGluValValThrLeuArgCysAsnHisArgAspAlaSerMetLeuGlySer 731
 QY 1285 CTGGGCTACAGATGCTGCTGATGTCAGTGTACTGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1344
 Db 732 LeuAlaTyrAsnValLeuLeuIleAlaLeuCysThrLeuTyrAlaPheLysThrArgLys 751
 QY 1345 GTGGCGGAGAGCTTCAACGAGCGCGAGCCCATCGGCTTCCATCATGTACACGACCTGCATT 1404
 Db 752 CysProGluAsnPheAsnGluAlaLysPheIleGlyPheThrMetTyrThrCysIle 771
 QY 1405 GTCTGGCTGGCTTCATCCCATCTCTTTTGGCACCTTCACAGTACGAGCGGAGGAGTGTAC 1464
 Db 772 IleTrpLeuAlaPheLeuProIlePheTyrValThrSerSerAsp-----TyrArg 788

Db 731 AsnVallyAspSerMetLeuIleSerLeuThrTyrAspValValLeuValIleLeu 750
QY 1315 TGTAAGTGTACGGCCATCAAGACCGGCGGTGGCCGAGACTTCAAGAGCGCCAAAGCC 1374
Db 751 CysThrValTyrAlaPheLysThrArgLysCysProGluAsnPheAsnGluAlaLysPhe 770
QY 1375 ATCGGCTTCACCATGTACACCACTGCAATTCCTGGCTGGCTTCATCCCATCTTTT 1434
Db 771 IleGlyPheThrMetTyrThrCysIleIleIleIlePheAlaPheLeuProIlePheTyr 790
QY 1435 GGCACCTCAGTCAGCCGACAAAGCTGTACATCCAGAACACCACTGACGGTCCGCTG 1494
Db 791 ValThrSerSerAsp-----TyrArgValGlnThrThrThrMetCysIleSerVal 807
QY 1495 AGTCGAGCGCTTCACTGCTCCCTGGGATGCTTACATGCCCAAGTCACTCATCTCTC 1554
Db 808 SerLeuSerGlyPheValValLeuGlyCysLeuPheAlaProLysValHisIleValLeu 827
QY 1555 TTCACACCGGAGCAAGCTGCCCAAGCGCAAGCGCAGCTCTCAAAGCGGTGGTCACCGCC 1614
Db 828 PheGlnProGlnLysAsn-----ValValThrHis 837
QY 1615 GCCACCATGTCCAAAGTTCCACAGAGAGGCG 1647
Db 838 ArgLeuHisLeuAsnArgPheSerValSerGly 848
RESULT 9
JC2132
metabotropic glutamate receptor 5 A - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2132
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131; MUID:94197696; PMID:7908515
A:Accession: JC2132
A:Molecule type: mRNA
A:Residues: 1-1180 <MIN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
F:580-604/Domain: transmembrane #1; receptor; transmembrane protein
F:617-637/Domain: transmembrane #status predicted <TM1>
F:644-664/Domain: transmembrane #status predicted <TM2>
F:694-714/Domain: transmembrane #status predicted <TM3>
F:738-759/Domain: transmembrane #status predicted <TM4>
F:773-794/Domain: transmembrane #status predicted <TM5>
F:803-827/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>
Alignment Scores:
Pred. No.: 2,128-65 Length: 1180
Score: 1123.00 Matches: 229
Percent Similarity: 58.88% Conservat: 106
Best Local Similarity: 40.25% Mismatches: 205
Query Match: 34.00% Indels: 29
Gaps: 8
US-10-828-332-6 (1-1755) x JC2132 (1-1180)
QY 7 GGGGTATCATCATCTTTCGCCAAGAGGATGACATCAGGGTTCGACCGGATCTTCTCCAGC 66
Db 324 GlyIleThrIleLysLeuGlnSerProAspVallyLysTyrPheAspTyrTyrLeuLys 343
QY 67 CGCAGCTGGACAAACAGCGGCAACATCTGGTTTGGCGAGTTCGGGAGGACAACTTC 126
Db 344 LeuArgProGluThrAsnHisArgAsnProTyrPheGlnGluPheTyrGlnHisArgPhe 363
QY 127 CATTCGAGTTGAGCGGCCCGCTCAAGAGGGAAGCCACATCAAGAGTGCACCAAC 186
Db 364 GlnCysArgLeuGluGlyPheProGlnGluAsnSerLysTyrAsnLysThrCysAsnSer 383
QY 187 CGAGAGCGCATCGGCGAGGACTCGCGCTTATGAGAGGAGGAGGAGGAGGAGGAGGAGG 246

Db 384 -----SerLeuThrLeuLysThrHisHisValGlnAspSerLysMetGlyPheValIle 401
QY 247 GAGCTGTGTACGGCCATGAGCGCCGCGCTGCGCCATGACCGCTGACCTGTGTCTCCGGC 306
Db 402 AsnAlaIleTyrSerMetAlaTyrGlyLeuHisAsnMetGlnMetSerLeuCysProGly 421
QY 307 CGGCTAGGACTCTGCCCTCGCATGGACCCGCTGGATGGACCCAGCTGCTTAACTATCATC 366
Db 422 TyrAlaGlyLeuCysAspAlaMetLysProIleAspGlyArgLysLeuLeuGluSerLeu 441
QY 367 AGGACCTCAACTCTCAGCATTCGGCGGAACCCCTGTAACCTTCAATGAGAACGGAGAC 426
Db 442 MetLysThrAsnPheThrGlyValSerGlyAspThrIleLeuPheAspGluAsnGlyAsp 461
QY 427 GCACCGGGCGCTACGACATCTACCATGAC-----CAACTGCGCAATGCTCGCGCGAGTAC 483
Db 462 SerProGlyArgTyrGluIleMetAsnPheLysGluMetGlyLysAspTyrPheAspTyr 481
QY 484 AAGGTCACTCGGCTCGTGAGACACCATCTGCACCTCAGAAATAGAGCGGATGACGTGCCA 543
Db 482 IleAsnValGlySerTrp---AspAsnGlyGluLeuLysMetAspAspGluValTrp 500
QY 544 GGGAGTGGCCAGAGTGGCGCGCTCCATCTGCAGTCTGCCCTGCGACGCGCGGAGGGA 603
Db 501 SerLysLysSerAsnIleIleArgSerValCysSerGluProCysGluLysGlyGlnIle 520
QY 604 AAGAAGACTGTGAAGGCG---ATGGCTTGTCTGGCACTGCGAGCCCTGCACCGGCTAC 660
Db 521 LysValIleArgLysGlyGluValSerCysCysTrpThrCysThrProCysLysGluAsn 540
QY 661 CAGTACCAGTGGACCGCTACACTGTAAAGACCTTGCCTCTACGACATGCGGCCCCACAGAG 720
Db 541 GluTyrValPheAspGluTyrThrCysLysAlaCysGlnLeuGlySerTrpProThrAsp 560
QY 721 AACCGCAGAGTGGCCAGCCCATCCCATCGTCAAGTTGAGTGGAGTGGCTGCCGTGGGCC 780
Db 561 AspLeuThrGlyCysAspLeuIleProValGlnTyrLeuArgTyrGlyAspProGluPro 580
QY 781 GTGTGCGCTCTTCTGCGCGGTGGTGGCATCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 581 IleAlaAlaValValPheAlaCysLeuGlyLeuLeuAlaThrLeuPheValThrValVal 600
QY 841 TTTGTGCGCTACAAACGATACCCCATCGTCAAGCGCTCGGGCGGGAACTGAGTCACTGCT 900
Db 601 PheIleIleTyrArgAspThrProValLysSerSerSerArgGluLeuCysTyrIle 620
QY 901 CTGCTGCGGGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 621 IleLeuAlaGlyIleCysLeuGlyTyrLeuCysThrPheCysLeuIleAlaLysProLys 640
QY 961 CTGGGGACCTGTTCTGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 641 GlnIleTyrCysTyrLeuGlnArgIleGlyIleGlyLeuSerProAlaMetSerTyrSer 660
QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGGGCAACCGTGGCTC 1080
Db 661 AlaLeuValThrLysThrAsnArgIleAlaArgIleLeuAlaGlySerLysLysLysIle 680
QY 1081 -----AGTGGCGCGCTTTCATCAGCGCGCGCTGCGAGTGGCCATCACCCTTCTCTC 1134
Db 681 CysThrLysLysProArgPheMetSerAlaCysAlaGlnLeuValIleAlaPheIleLeu 700
QY 1135 ATCTCCCTGCGAGTCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
Db 701 IleCysIleGlnLeuGlyIleIleValAlaLeuPheIleMetGluProProAspIleMet 720
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Db 721 HisAspTyr-----ProSerIleArgGluValTyrLeuIleCys 733
QY 1255 GACATCTCGGACCTGCTCCCTCATCTGCTGCTGGGCTGACAGCATGCTGCTGCTGCTGCTG 1314
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Db 660 AlaLeuValThrLysThrAsnArgIleAlaArgIleLeuAlaGlySerLysLysLysIle 679
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Db 680 CysThrLysLysProArgPheMetSerAlaCysAlaGlnLeuValIleAlaPheIleLeu 699
QY 1135 ATCTCCCTGCAGCTCTCGGCATCGCTGTGTGTTGTTGGTGGAGCCCTCCCACTCGGTG 1194
Db 700 IleCysIleGlnLeuGlyIleValAlaLeuPheIleMetGluProProAspIleMet 719
QY 1195 GTGGACTTCCAGACCAACGACACTTGACCCCGCTTTCAGGGGGCTGCTCAAGTGC 1254
Db 720 HisAspTyr-----ProSerIleArgGluValTyrLeuIleCys 732
QY 1255 GACATCTCGGACTGCTCCCTCATCTGCTGCTGGCTACAGATGCTGCTGATGGTCAG 1314
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Db 753 CysThrPheTyrAlaPheLysThrArgAsnValProAlaAsnPheAsnGluAlaLysTyr 772
QY 1375 ATCGGCTTCCACCATACACCACTGCAATGTGTGGCTGGCTTCATCCCATCTCTTTT 1434
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QY 1435 GGCACCTCACAGTCAGCGCAGCTGTATCATCCAGACCAACCACTGACCGTCTCCGTG 1494
Db 793 GlySerAsn-----TyrIleIleIleThrMetCysPheSerVal 805
QY 1495 AGTCGAGCGCTTCACTGCTGCTGGGATGCTTACATGCCCAAGTCTACATCATCTC 1554
Db 806 SerLeuSerAlaThrValAlaLeuGlyCysMetPheValProLysValTyrIleLeu 825
QY 1555 TTCCACCCGGAGCAGAGTGTGCCAAGCGCAGCGACTCTCAAGCGGTGGTGGTCCGCC 1614
Db 826 AlaLysProGluArgAsnVal-----ArgSerAlaPheThrThr 838
QY 1615 GCACCATGTCCACCAAGTTCCACAGAGGGCACTTCAGGCCCAATGGGGAGCCAAA 1674
Db 839 SerThrValValArgMetHisValGlyAspGlyLys-SerSerSerAlaAlaSerArgSe 858
QY 1675 TCAGAGCTGTGTGAGAACTGGAGA 1699
Db 858 rSerSerLeuValAsnLeuThrPlys 866

RESULT 13
S71376
glutamate receptor homolog - cherry salmon
C:Species: Oncorhynchus masou (cherry salmon)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S71376
R:Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
FBS Lett. 392, 71-76, 1996
A:Title: Cloning and characterization of a bifunctional metabotropic receptor activated
A:Reference number: S71376; MUIB:96354880; PMID:8769318
A:Accession: S71376
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1218 <KUB>
A:Cross-references: UNIPROT:Q902F3
C:Keywords: glycoprotein; phosphoprotein
F:603-625/Domain: transmembrane #status predicted <TM1>
F:640-660/Domain: transmembrane #status predicted <TM2>
F:672-690/Domain: transmembrane #status predicted <TM3>
F:717-737/Domain: transmembrane #status predicted <TM4>
F:761-782/Domain: transmembrane #status predicted <TM5>
F:796-817/Domain: transmembrane #status predicted <TM6>
F:826-850/Domain: transmembrane #status predicted <TM7>
F:104,233,403,525,757/Binding site: carbohydrate (Asn)
F:636,697,961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pre
F:705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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F:892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predic
Alignment Scores:
Pred. No.: 7.61e-65 Length: 1218
Score: 1114.50 Matches: 220
Percent Similarity: 60.15% Conservative: 97
Best Local Similarity: 41.75% Mismatches: 189
Query Match: 33.74% Indels: 21
Gaps: 7
DB: 2

US-10-828-332-6 (1-1755) x S71376 (1-1218)
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QY 67 CGCAGCTGGACAAACAGCGGCAACATCTGGTTTCCGAGTTCTCGGAGGACAACTTC 126
Db 367 LeuArgLeuAsnThrAsnThrArgAsnProTyrPheProGluPheThrGlnHisArgPhe 386
QY 127 CATTGCAAGTTGACCCCGCCGCTCAAGAGGGAAGCCACATCAAGAAGTGCACCAAC 186
Db 387 GlnCysArgIleProGlyHisProLeuGluAsnMetAsnTyrArgLysAsnCysSerGly 406
QY 187 CGAGAGCGCATCGGCGAGGACTCGGCTTATGAGCAGGAGGGGAAAGTGCAGTTCGTGATT 246
Db 407 TyrGluSerLeu-----GluAspAsnTyrValGlnAspSerLysMetGlyPheValIle 424
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Db 445 HisValGlyLeuCysLysAlaMetAspProIleAspGlySerGlnLeuLeuGluPheLeu 464
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Db 465 MetArgThrSerPheThrGlyValSerGlyGluAspValTyrPheAspGluAsnGlyAsp 484
QY 427 GCACCGGGGCTACGACATCTACAGTACCA---CTGGCAATGGCTCGGCGAGTAC 483
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QY 484 AAGGTATCGCTCGTGCAGACACCACTGCACCTCAGAAATAGAGCGGATGACAGTGGCCA 543
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QY 604 AAGAAGACTGTGAAGGGC---ATGGTGTGCTGCTGGCACTCGCGAGCCCTGCACCGGTAC 660
Db 544 LysValIleArgLysGlyGluValSerCysCysTrpIleCysThrAlaCysLysAspAsn 563
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Db 564 GluIleValGlnAspGluPheThrCysThrAlaCysAspLeuGlyTyrTrpProAspPro 583
QY 721 AACCGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGAGCTCGCCGTGGGCC 780
Db 584 GluLeuGluGlyCysGluProIleThrLeuArgTyrLeuGluTyrGlyAsnProGluSer 603
QY 781 GTGCTGCCCTCTTCTGCGCGTGGTGGCATCCGCCAGCTGCTGCTGGTGGTGTACAG 840
Db 604 IleValGlnValValPheAlaCysLeuGlyIleLeuValThrSerPheValThrPheIle 623
QY 841 TTTGTGCGCTACAACGATACCCCATCGTAAAGCCCTCGGGCCGGGAACCTGAGCTACGTG 900
Db 624 PheValLeuTyrArgAspThrProValLysSerSerSerArgGluLeuCysTyrIle 643
QY 901 CTGCTGGCGGGCATCTTTTCTGTGTACGCCCACTACCTTCTCATGATCGCAGAGCCGGAC 960
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Db      644  ILeuAlaGlyIlePheLeuGlyTyrIleCysProPheThrLeuIleAlaGlnProThr 663
QY      961  CTGGGACCTGTTCTCGTCCGCGCATCTTCTTAGGCTCGGCATGAGCATCACTACGGC 1020
Db      664  ValAlaSerCysTyrLeuGlnArgLeuLeuValGlyLeuSerAlaThrMetCysTyrSer 683
QY      1021  GCCTCTGACCAAGACCAACCCATTTACCGCATCTTGGAGCGGCAACCGTCGGTC 1080
Db      684  AlaLeuValThrLysThrAsnArgIleAlaArgIleLeuAlaGlySerLysLysIle 703
QY      1081  AGTGCC-----CGGGTTTCATCAGCCCGCTCGCAGCTGCGCATCACTTCATCCTC 1134
Db      704  CysThrArgLysProArgPheMetSerAlaTrpAlaGlnLeuValIleAlaGlyLeuLeu 723
QY      1135  ATCTCCTCGAGTGTCTCGCATCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1194
Db      724  ValSerValGlnLeuThrLeuGluValThrLeuIleIleLeuGluProMetProVal 743
QY      1195  GTGGACTTCAGGACCAACGACACTTGTGACCCCGCTTTGCCAGGGCGGTGTCAAGTGC 1254
Db      744  LysSerTyr-----ProSerIleArgGluValPheLeuIleCys 756
QY      1255  GACATCTCGGACTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1314
Db      757  AsnThrSerThrValGlyMetValAlaProLeuGlyTyrAsnGlyLeuLeuIleMetSer 776
QY      1315  TGTACTGTGTACGCCATCAAGACCCGAGCGTCCCGAGACCTTCAACGAGGCGCAAGCCC 1374
Db      777  CysThrTyrTyrAlaPheLysThrArgAsnValProAlaAsnPheAsnGluAlaLysTyr 796
QY      1375  ATGGCTTCACCATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1434
Db      797  IleAlaPheThrMetTyrThrThrCysIleIleIleIleIleIleIleIleIleIle 816
QY      1435  GGCACCTCAGCTCAGCCGACAGCTGTATATCCAGACCAACCACTGACGCTCTCCGTC 1494
Db      817  GlySerAsn-----TyrLysIleIleIleIleIleIleIleIleIleIleIleIle 829
QY      1495  AGTCTGAGCGCTTCACTGCTCCCTGCGGATGCTTACATCCCAAGCTTACATCATCTTC 1554
Db      830  SerLeuSerValThrValAlaLeuGlyCysMetPheSerProLysIleIleIleLeu 849
QY      1555  TTCACCCGAGCAGAACGTG 1575
Db      850  AlaLysProGluArgAsnVal 856

RESULT 14
T27628
hypothetical protein ZC506.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27628
R:Harris, B.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z20395
A:Accession: T27628
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-999 <MIL>
A:Cross-references: UNIPROT:Q09630; EMBL:Z47073; PIDN:CAA87374.1; GSPDB:GN00028; CESP:ZC
A:Experimental source: clone ZC506
C:Genetics:
A:Gene: CESP:ZC506.4
A:Map position: X
A:Introns: 32/2; 65/3; 77/3; 113/2; 140/3; 177/2; 240/2; 277/1; 315/2; 439/2; 471/3; 591
C:Superfamily: metabotropic glutamate receptor 4

Alignment Scores:
Pred. No.: 1,04e-56 Length: 999
Score: 989.50 Matches: 223
Percent Similarity: 52.33% Conservative: 102
Best Local Similarity: 35.91% Mismatches: 211

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Query Match: 29.96% Indels: 85
DB: Gaps: 17
US-10-828-332-6 (1-1755) x T27628 (1-999)
QY      22  TTGCCAACGAGGATGACATCAGGGTTTCGACCGATCTCTCCAGC-----CGCACGCTG 75
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QY      76  GACAAACACAGCGCAACATCTGCGGTTTTCGAGATTCTGGAGGACCACTTCCATTCGAAG 135
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QY      136  TTGAGCCGCCACGCGCTCAAGAAAGGAGCCATCAAGAGTGACCAACCGAGAGCGC 195
Db      429  PheAsp-----ThrProGlySerThrAlaSerArgCys-----GluAap 442
QY      196  ATCGGCGGAGGACTCG---GCCTATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 252
Db      443  IleLysGlnSerThrGluGlyPheAsnAlaAspAspLysValGlnPheValIleAspAla 462
QY      253  GTGTACGCGCATCGGCGCAGCGCTGACGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCT 306
Db      463  ValTyrAlaIleAlaHisGlyLeuGlnSerMetLysGlnAlaIleCysProAspAspAla 482
QY      307  -----CGGTTAGGACTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 333
Db      483  IleGluAsnHisTrpIleSerArgTyrSerLysGlnProGluIleCysHisAlaMetGln 502
QY      334  CCGCTGGATGGACCCAGCTGTTAAG---TACATCAGGAAGAGTCACTTCTCAGCGC--- 387
Db      503  AsnIleAspGlySerAspPheTyrGlnAsnTyrLeuLeuLysValAsnPheThrLysLys 522
QY      388  -----AATGGCTGCGCGGACCCCT 402
Db      523  ThrIleSerIlePheSerSerPheArgLeuSerProPheSerAspIleValGlyLysArg 542
QY      403  GTAACCTTTCAATGAGAACGAGACCGACCGGGCGCTACGACATCTTACAGTACCAACTG 462
Db      543  PheArgPheSerProGlnGlyAspGlyProAlaSerTyrThrIleLeuThrTyrLysPro 562
QY      463  CGC-----AATGGCTGCGCGGACGATCAAG 486
Db      563  LysSerMetAspLysLysArgMetThrAspAspGluSerSerProSerAspTyrVal 582
QY      487  GTCATCGGCTCGTGACAGACACCTGACCTCAGAAATAGAGCGGATGACGTCGCGCAGG 546
Db      583  GluIleGlyHisTrpSerGluAsnAsnLeuThrIleTyrGluLysAsnLeuTrp---Tyr 601
QY      547  AGTGCCAGCAGCTCCGCGCTCCATCTGCACTGCTGCGCTGCGCTGCGCTGCGCTGCGCT 606
Db      602  AspProAspHisThrProValSerValCysSerLeuProCysLysIleGlyPheArgLys 621
QY      607  AAGACTGTGAGGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
Db      622  GlnLeuIleLysAspGluGlnCysCysTrpAlaCysSerLysCysGluAspTyrGluTyr 641
QY      667  CAAGTGGACCGCTACACCTGTAAAGACCTGCGCTCAGCATCGCGCCACAGAACCGC 726
Db      642  LeuIleAsnGluThrHisCysValGlyCysGluGlnGlyTyrTrpTrpThrLysAspArg 661
QY      727  ACGAGCTGCCAGCCCATCCCTCAAGTTGGAG-----TGGAGCTCGCGCTGG 777
Db      662  LysGlyCysPheAspLeuSerLeuSerGlnLeuLysTyrMetArgTrpArgSerMetTyr 681
QY      778  GCGGTGCTGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
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QY      838  ACGTTTGTGCGCTACACGATACCCCATCGTCAAGGCTCGGCGCGGAGCACTGAGCTAC 897
Db      702  ValTyrValIleTyrAsnGluThrProValLysAlaSerGlyArgGluLeuSerTyr 721

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42	Ser	Arg	Thr	Leu	Asp	Asn	Asn	Arg	Asn	Ile	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Asp	Asn	61			
124	TTC	CAT	TGC	AAG	TGT	GAC	CGC	CGC	CA	GAG	GGG	AA	GCG	CA	CAT	CA	AGA	AGT	GC	ACC	183		
62	Phe	His	Cys	Leu	Ser	Arg	His	Ala	Leu	Leu	Val	Ser	Gly	Ser	His	Ile	Val	Ser	Cys	Thr	81		
184	AAC	CGA	GCG	CGC	AT	CGG	CGC	AGG	ACT	CGC	CC	TAT	CAG	CAG	GAG	GGG	AA	GAG	TGC	AGT	TCGTG	243	
82	Asn	Arg	Glu	Arg	Ile	Gly	Gln	Asp	Ser	Ala	Tyr	Glu	Gln	Glu	Gly	Val	Gln	Phe	Val		101		
244	ATT	GAC	CTG	TGT	ATC	GCC	ATG	GGG	CC	ACG	CGC	TGC	ACG	CC	ATG	CA	CGT	GAC	CTG	TGT	CC	303	
102	Ile	Asp	Ala	Val	Tyr	Ala	Met	Gly	His	Ala	Leu	His	Ala	Met	His	Arg	Asp	Leu	Cys	Pro	121		
304	GGC	CGC	TAG	CAT	CTC	CGC	CTC	GAT	CGG	AC	CCG	TGC	ATG	GGC	AC	CCG	AGT	CGT	CTT	AAG	TAC	363	
122	Gly	Arg	Val	Gly	Leu	Cys	Pro	Arg	Met	Asp	Pro	Val	Asp	Gly	Thr	Gln	Leu	Leu	Val	Ser	Tyr	141	
364	ATC	AGG	AA	CGT	CA	ACT	TCT	CAG	GAT	TGC	GGG	AA	CC	CT	TAA	CC	TTC	AT	GAG	AA	CGG	423	
142	Ile	Arg	Asn	Val	Asn	Phe	Ser	Gly	Ile	Ala	Gly	Asn	Pro	Val	Thr	Phe	Asn	Glu	Asn	Gly	161		
424	GAC	CA	CCG	GGG	CGC	TAC	GAT	TCT	ACC	AGT	TAC	CA	ACT	GC	CA	AT	TGC	CA	AT	TGC	CGC	CGG	483
162	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Tyr	Gln	Tyr	Gln	Leu	Arg	Asn	Gly	Ser	Ala	Glu	Tyr	181		
484	AAG	TCA	TC	CGC	TCT	CGG	AC	AGC	CA	CC	CTC	GAT	CGC	CA	CTC	AG	AT	GAG	CGG	ATG	CGC	CA	543
182	Lys	Val	Ile	Gly	Ser	Trp	Thr	Asp	His	Leu	His	Leu	Arg	Ile	Glu	Arg	Met	Gln	Trp	Pro	201		
544	GGG	AGT	GGC	CAG	CAG	CTC	CGC	CGT	TCC	ATC	TGC	AGT	CTG	CC	CTG	CC	AC	GCG	CGG	CGG	AG	CGG	603
202	Gly	Ser	Gly	Gln	Gln	Leu	Pro	Arg	Ser	Ile	Cys	Ser	Leu	Pro	Cys	Gln	Pro	Gly	Glu	Arg	221		
604	AAG	AAG	ACT	GTG	AA	GCG	CAT	GGC	TGT	GCT	GTC	CA	CTG	CG	AC	TGC	AG	CGC	CGT	ACC	AG	663	
222	Lys	Val	Thr	Val	Lys	Gly	Met	Ala	Cys	Cys	Trp	His	Cys	Glu	Pro	Cys	Thr	Gly	Tyr	Gln	241		
664	TAC	CA	AAG	TGC	ACG	CTA	CA	CTG	TAA	AGC	TGC	CC	CTC	TAC	GAC	ATG	CGG	CGG	CGC	CAG	AG	723	
242	Tyr	Gln	Val	Asp	Arg	Tyr	Thr	Cys	Lys	Thr	Cys	Pro	Tyr	Asp	Met	Arg	Pro	Thr	Glu	Asn	261		
724	CGC	AC	GAG	CTG	CC	AGC	CC	AT	CCCC	AT	CGT	CA	AGT	TTC	GAG	TGG	GA	CTC	CGC	CGT	GGG	CGG	783
262	Arg	Thr	Ser	Cys	Gln	Pro	Ile	Pro	Ile	Val	Lys	Leu	Glu	Trp	Asp	Ser	Pro	Trp	Ala	Val	281		
784	CTG	CCC	CTT	CTT	CGC	CGC	TGT	GGG	AT	CCG	CC	CA	CGT	TGT	TGC	TGT	GGT	GC	AGT	TTT	843		
282	Leu	Pro	Leu	Phe	Leu	Ala	Val	Val	Gly	Ile	Ala	Ala	Thr	Leu	Phe	Val	Val	Val	Thr	Phe	301		
844	GTG	CGC	TAC	AA	CG	AT	AT	CCCC	AT	CGT	CA	AGC	CTC	GGG	CGG	CA	ATG	ACT	AGT	CGT	CTG	903	
302	Val	Arg	Tyr	Asn	Asp	Thr	Pro	Ile	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	Leu	321		
904	CTG	CGG	GGC	AT	CTT																		

Db	402	GlnLeuLeuGlyLeCysValTrpPheValValAspProSerHisSerValValAspPhe	421
Qy	1204	CAGGACCAACGGACACTTGACCCCGCTTTGGCCAGGGGGCTGTCTCAAGTCGCACTCTCG	1263
Db	422	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLeuLeuLeuLeuSer	441
Qy	1264	GACCTGTCCCTCATCTGCTGCTGGGCTACAGCATCTGCTGATGTGTACAGTGTACTGTG	1323
Db	442	AspLeuSerLeuLeuLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal	461
Qy	1324	TAGCCATCAAGACCGGAGCGCGCCGAGAGCTTCAACGAGGCGCAAGCCCATCGGCTTC	1383
Db	462	TyAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	481
Qy	1384	ACCATGTACACCACTGCATTGTCTGGCTGGCTTCATCCCCATCTTTTGGCACCTCA	1443
Db	482	ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer	501
Qy	1444	CAGTCAGCCGACAAAGCTGTACATCCAGAACACACACTGACGGTCTCCGTGAGTCTGAGC	1503
Db	502	GlnSerAlaAspIysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer	521
Qy	1504	GCCTCAGTGCCTCGGGGATGCTCTACATGCCCAAGTCTTACATCATCTCTTCCACCCG	1563
Db	522	AlaSerValSerLeuGlyMetLeuTyrMetProIysValTyrIleLeuLeuPheHisPro	541
Qy	1564	GAGCAGAACGTGCCCAAGCGCAGCTCTCAAAGCCGTGTCTACCGCGCCACCATG	1623
Db	542	GluGlnAsnValProIysArgIysArgSerLeuLeuAlaValValThrAlaAlaThrMet	561
Qy	1624	TCCAACAAGTTCACACAGAGGGCAACTTCAGGCCCAATGGGGAGGCCAAATCAGAGCTG	1683
Db	562	SerAsnIysPheThrGlnIysGlyAsnPheArgProAsnGlyGluAlaIysSerGluLeu	581
Qy	1684	TGTGAGNACTGAGACGCCCGCGCTGTACCAACAGACACTACGTCTACCTACCTACCAAC	1743
Db	582	CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn	601
Qy	1744	CATGCCCATC 1752	
Db	602	HisAlaIle 604	
RESULT 2			
PCT-US91-09422-19			
; Sequence 19, Application PC/TUS9109422			
; GENERAL INFORMATION:			
; APPLICANT: Mulvihill, Eileen R.			
; APPLICANT: Hagen, Frederick S.			
; APPLICANT: Houamed, Khaled M.			
; APPLICANT: Almers, Wolfhard			
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS			
; NUMBER OF SEQUENCES: 33			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend			
; STREET: One Market Plaza, Steuart Street Tower			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94105-1492			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: PCT/US91/09422			
; FILING DATE: 19911212			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/672,007			
; FILING DATE: 18-MAR-1991			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/648,481			

QY		723	TACCAAGTGGACCGCTACACCTGTAAAGACTGCCCTCTACGACATCGCGGCCACAGAGAAC	
Db		550	TyrGlnValAspArgTyThrCysIysThrCysProTyzAspMetArgProThrGluAsn	569
QY		724	CGCACGAGTCGCACGACCATCCCATCTGCAAGTTGGAGTGGAAGTTCGGCCGTGGGCGCGTG	783
Db		570	ArgThrSerCysGlnProIleProlIeValIysLeuGluTrpAspSerProTrpAlaVal	589
QY		784	CTGCCCTCTTCTCGCGCGTGGTGGGCATCGCCGCGCAGCTGTCTCGTGGTGGTACAGTTT	843
Db		590	LeuProLeuPheLeuAlaValVaIGlyIleAlaAThrLeuPheValValThrPhe	609
QY		844	GTGGCTACAACGATACCCCCATCGTCAAAGCCTCGGGCCGGGAAGTGAAGTACGTGCTG	903
Db		610	ValArgTyzAsnAspThrProIleValIysAlaSerGIyArgGluLeuSerTyzValLeu	629
QY		904	CTGGCGGGCATCTTCTGTGTGTACGCCACTACTCTTCATCATCGACAGCGGACCTG	963
Db		630	LeuAlaGIylIlePheLeuCysTyzAlaThrPheLeuMetIleAlaGluProAspLeu	649
QY		964	GCGACCTGTTCGCTCGCGCGCATCTTCTTAGGGCTCGGCATGAGCATCAGCTACGCGGCC	1020
Db		650	GlyThrCysSerLeuArgArgIlePheLeuGIyLeuGIyMetSerIleSerTyzAlaAla	669
QY		1024	CTGCTGACCAAGACAACCGCATTTTACGCATCTTTTGAGCAGGGCAACCGTCGTCAGT	1080
Db		670	LeuLeuThrTyzThrAsnArgIleTyzArgIlePheGluGlnGIyLysArgSerValSer	689
QY		1084	GCCC CGGTTTTATCAGCCCCCGCTCGAGCTGGGCATCACCTTCATCTCATCTCCCTG	114
Db		690	AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSerLeu	709
QY		1144	CAGCTGCTCGGCATCTGGGTGTGTCTGGTGGACCCCTCCACTCGGTGGTGGACTTC	120
Db		710	GlnLeuLeuGIyllIeCysValTrpPheValValAspProSerHisSerValValAspPhe	729
QY		1204	CAGAACCAACGACACTTGCACCCCGCTTTCAGGGCGGTGCTCAAGTGGACATCTCG	126
Db		730	GlnAspGlnArgThrLeuAspProArgPheAlaArgGIyValLeuLysCysAspIleSer	749
QY		1264	GACCTGTCCCTCATCTGCCTCTGGCTTACAGCATGCTGTCATGGTCAAGTGTACTGNG	132
Db		750	AspLeuSerLeuIleCysLeuLeuGIyTyzSerMetLeuLeuMetValThrCysThrVal	769
QY		1324	TACGCCATCAAGACCCGAGGCGTCCCCGAGACCTTCAACAGGCCAAGCCCATCGGCTTC	138
Db		770	TyrAlaIleIysThrArgGIyValProGluThrPheAsnGluAlaIysProIleGlyPhe	789
QY		1384	ACCATGTACACCACTGCATTGTCTGGTGCCTTCATCCCCCATCTTTTGGCACCTCA	144
Db		790	ThrMetTyzThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGIyThrSer	809
QY		1444	CAGTCAGCCGACAGCTGTATCATCCAGACAACCACTGACGGTCTCGGTGAGTCTGAGC	150
Db		810	GlnSerAlaAspLysLeuTyzIleGlnThrThrThrLeuThrValSerValSerLeuSer	829
QY		1504	GCTTCAGTGTCCCTGGGATGCTCTACATGCCCCAAGTCTACATCATCTCTTCCACCCG	156
Db		830	AlaSerValSerLeuGIyMeLeuTyzrMetProLysValTyzIleLeuPheHisPro	849
QY		1564	GAGCAGAACGTGCCCAAGCGCAGCTCTCAAAGCCGTGGTCAACGCCGCCACCATG	162
Db		850	GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet	869
QY		1624	TCCAACAGTTTCACACAGAGGGCACTTCAGGCCCAATGGGAAGCCNAATCAGAGCTG	168
Db		870	SerAsnLysPheThrGlnLysGIyAsnPheArgProAsnGIyGluAlaIySSerGluLeu	889
QY		1684	TGTGAGACCTGGAGACCCAGCGCTGGCTACCAACAGACCTACGTCACTTACCTACCAAC	174
Db		890	CysGluAsnLeuGluThrProAlaLeuAlaThrLysGlnThrTyzValThrTyzThrAsn	909
QY		1744	CATGCCATC 1752	

US-10-828-332-6 (1-1755) x PCT-US91-09422-19 (1-912)

QY	7	GGGTTATCATCATCTTTGGCAACGAGGATGACA---TCAGGGTTTCGACCGCATCTTCTCC	63
Db	330	GiYaLaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer	349
QY	64	AGCGCGACGCTCGACAACAACAGGCGCAACATCTGGTTTGCAGAGTTCTCGGAGGACAAC	123
Db	350	SerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn	369
QY	124	TTCCATTGCAAGTTGAGCGGCCACCGCTCTCAAGAAGGGAAGCCACATCAAGAAGTGCCACC	183
Db	370	PheHisCysLeuSerArgHisAlaLeuLeuLysGlySerHisIleLeuLysCysThr	389
QY	184	AACCGAGACGCGATCGGCGAGGACTCGCGCTTATGAGCAGGAGGGGAAGGTGCAGTTTCGTG	243
Db	390	AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal	409
QY	244	ATTGACGCTGTGTAGCCCATGGCCATGGCCACGCGCTGCACGCCCATGCACCGTGTGTCCC	303
Db	410	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	429
QY	304	GGCGCGGTAGGACTCTGCGCTCGCATGACACCCGCTGATGGCACCACGCTGCTTAGGTAC	363
Db	430	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr	449
QY	364	ATCAGGAACGTCCAATTCTTCAGGCATTTCGGGGGAACCTGTAACTTCAATGAGAAGCGGA	423
Db	450	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	469
QY	424	GACGACCGGGCGGTACGACATCTTACAGTACCAACTTCGCGCAATGCTCGCGCGAGTAC	483
Db	470	AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr	489
QY	484	AGGTCATCGGCTCTGTGACGACACACCTGCACCTCAGATAGAGCGGATGCAGTGCACA	543
Db	490	LysValIleGlySerTrpThrAspHisIleuHisIleuArgIleGluArgMetGlnTrpPro	509
QY	544	GGGAGTGGCCACGACGTGCGCGCTTCCATCTTCGAGTCTTGCCCTGCCACCGCGGGAGCGGA	603
Db	510	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	529
QY	604	AGAAGACTGTGAAGGGCAGTGTGCTGTGGCATCTGCAGACCCCTGCACCGGGTACCAG	663
Db	530	LysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysTrpGlyTyrGln	549

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Db          910 HisAlaIle 912
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RESULT 3
US-08-617-785-2
; Sequence 2, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-2

Alignment Scores:
Pred. No.:          9,638-236      Length:          912
Score:              3004.50        Matches:         564
Percent Similarity: 97.77%         Conservative:    6
Best Local Similarity: 96.74%       Mismatches:      12
Query Match:        90.96%         Indels:           1
Db:                  3              Gaps:             1

US-10-828-332-6 (1-1755) x US-08-617-785-2 (1-912)
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QY      64 AGCCGACGCTGGACAAACAGCGCCAACTCTGGTTTGGCGAGTTCTGGAGAGACAAC 123
Db      350 SerArgThrLeuAspAsnArgAsnIleTTPheAlaGluPheTrpGluAspAsn 369
QY      124 TTCATTGCAAGTTAGCGGCCACCGCTCAAGAGGGAAGCCACATCAAGAGTGCACC 183
Db      370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysCysThr 389
QY      184 AACCGAGAGCGCATCGGCGAGACTCGCGCTATGAGCAGGAGGGAAGCTGCAGTTCGTG 243
Db      390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
QY      244 ATTGACGCTGTGTACGCCATGGCCACGCGCTGCAAGCCATGCACCGCTGTGTCCC 303
Db      410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
QY      304 GCGCCGCTAGGACTCTGCCCTCGCATGGACCCCGTGGATGGACCCAGCTCTTAAGTAC 363
Db      430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLysTyr 449
QY      364 ATCAGGAAGCTCAACTCTCAGGCAATCGGGGAACCTGTAAACCTTCAATGAGAACGGA 423
Db      450 IleArgAsnValAsnPheserGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
QY      424 GACGACCGGGCGCTACGACATCTTACAGTACCAACTCGCAATGGCTCGGCCGAGTAC 483
Db      470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
QY      484 AAGGTTCATCGCTCGTGACAGACCACCTGCACCTCAGAATAGAGCGATGCAGTGGCCA 543
Db      490 LysValIleGlySerTrpThrAspHisLeuArgIleGluArgMetHisTrpPro 509
QY      544 GGGAGTGGCCAGCAGCTGCCCGCTCCATCTGCAGTCTGCCCTGCCAGCCCGGGAGCGA 603
Db      510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
QY      604 AAGAGACTGTGAAGGCGATGGCTTGCTGGCACTGGCAGCCCTGCACCGGCTACCAG 663
Db      530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
QY      664 TACCAGTGCAGCCCTACACTGTAAAGACTGCCCTTACGACATGCGGCCACACAGAGAAC 723
Db      550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
QY      724 CGCAGCAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCCCGTGGCCGTG 783
Db      570 ArgThrGlyCysArgProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
QY      784 CTGCCCTCTTCTGGCGGTGGGCGATCGCCCGCAGCTGTTCGTGGTGGTTCACGTTT 843
Db      590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
QY      844 GTGCGCTACAACGATACCCCATCGTCAAGCGCTCGGGCGGGGAACCTGAGTACGTGCTG 903
Db      610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
QY      904 CTGCGGGGCTCTTTCTGTGTAGCCCACTACCTTCTCATGTATGAGAGCCGAGACTG 963
Db      630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
QY      964 GGGACCTGTTCGCTCCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGTACGCGGCC 1023
Db      650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
QY      1024 CTGCTGACCAAGCAACCGCATTTACCGCATCTTTTCAGCAGGAGGCAACCGTCCGTCAGT 1083
Db      670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
QY      1084 GCGCGCGTTTCATCAGCCCGCGCTCGCAGCTGCCATCACCTTTCATCTCATCTCCCTG 1143
Db      690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
QY      1144 CAGCTGCTGGCATCTCGGTGTGGTTCGTGGTGAGACCCCTCCCACTCGGTGGTGGACTTC 1203
Db      710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY      1204 CAGGACCAACGACACCTTGACCCCGCTTTGCCAGGCGGTGCTCAAGTGCAGATCTCG 1263
Db      730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY      1264 GACTGTCCCTCATCTCCCTGCTGGGTACAGCATGCTGTGATGTGTCACGTGTACTGTG 1323
Db      750 AspLeuSerLeuIleCysLeuLeuGlyTyr-SerMetLeuLeuMetValThrCysThrVal 769
QY      1324 TAGCCCATGAGACCCCGAGCGGTCCCGAGACCTTCAACGAGGCCAAGCCCATCGGCTTC 1383
Db      770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY      1384 ACCATGTACACCACTCTGCTGGCTGGCTTTCATCCCATCTTTTGGCACCTCA 1443
Db      790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
QY      1444 CAGTCAGCCGCAAGCTGTATCATCCAGACCAACACACTGACGCGTCTCCGTGAGTCTGAGC 1503
Db      810 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 829
QY      1504 GCTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAGCTTACATCATCTCTTCCACCCG 1563
Db      830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
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QY 1564 GAGCAGACGTCCCAAGCGCAGCGAGCTCTCAAGCGGTGGTCAACCGCGCCACCATG 1623
Db |||||
850 GluGlnAsnValProLysArgLysSerLeuLysAlaValThrAlaAlaThrMet 869
QY 1624 TCAACAAGTTTACACAGAGGCGCACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
Db |||||
870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACTGTGAGACCCAGCGCTGTGCTACCAACAGACCTTACCTACCAAC 1743
Db |||||
890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
QY 1744 CATGCCATC 1752
Db |||||
910 HisAlaIle 912

RESULT 4

US-09-641-318-2
; Sequence 2, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; ; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS

; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: GAYLO, PAUL J.

; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEX: (317) 276-3861

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 912 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-641-318-2

Alignment Scores:

Pred. No.: 9.63e-236 Length: 912
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 90.96% Indels: 1
DB: 3 Gaps: 1

US-10-828-332-6 (1-1755) x US-09-641-318-2 (1-912)

QY 7 GGGGTATCATCATCTTTGGCAACGAGGATGACA---TCAGGGTTGACCGATACCTCTCC 63
Db |||||
330 GlyAlaValThrIleLeuProLysArgMetSerValArgPheAspArgTyrPheSer 349

QY 64 AGCCGACGCTGGACAAACAAACAGGCGCAACATCTGTTTCCGAGTTCTTGGAGAGCAAC 123
Db |||||
350 SerArgThrLeuAspAsnAsnArgAsnIleTrrPheAlaGluPheTrrPheGluAspAsn 369
QY 124 TTCCATTTCAGTTGAGCGCCGACCGCTCAAGAGGGAAGCCACATCAAGAGTGCACC 183
Db |||||
370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysCysThr 389
QY 184 AACCCAGAGCGCATCGGCGAGACTCGGCTTATGAGCAGAGGAGGAAAGTGCAGTTCTG 243
Db |||||
390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal 409
QY 244 ATTGACGCTGTGTACGCCATGCGCGCTGCAGCCATGCACCTGCACCTGCTGTGCTCC 303
Db |||||
410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
QY 304 GCGCGGTAGGACTCTGCGCTCGCATGGACCCCGGTGGATGGCACCCAGCTGCTTAAGTAC 363
Db |||||
430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
QY 364 ATCAGGAACGTCAACTTCTCAGGCAATGCGGGGAACCCCTGTAACTTCAATGAGAAGCA 423
Db |||||
450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
QY 424 GAGCACCGGCGCTACGACATCTACAGTACCACTGCGCAATGGCTCGGCGCGAGTAC 483
Db |||||
470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
QY 484 AGGTCTCATGCTCGTGAGACACCACTGCACCTCAGATAGAGGAGGAGTGCAGTGGCCA 543
Db |||||
490 LysValIleGlySerTrrThrAspHisLeuHisLeuArgIleGluArgMetHisTrrPro 509
QY 544 GGGAGTGGCAGCAGCTGCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCGCGGAGCA 603
Db |||||
510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
QY 604 AAGAAGCTGTGAAGGGCATGCTTGTCTGGCACTCGAGCCCTGCACCGGGTACCCAG 663
Db |||||
530 LysLysThrValLysGlyMetProCysCysTrrHisCysGluProCysThrGlyTyrGln 549
QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATGGGCGGCCACAGAAC 723
Db |||||
550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
QY 724 CGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGCGGGCGGTG 783
Db |||||
570 ArgThrGlyCysArgProIleIleLysLeuGluTrrPglySerProTrrPalaVal 589
QY 784 CTGCCCCCTTCTTCTGGCGTGGTGGCATCGCCGACCTGCTGCTGCTGCTGCTGCTGCT 843
Db |||||
590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
QY 844 GTGCGCTACACGATACCCCATCGTCAAGGCTCGGCGCGGAACTGAGCTACGCTGCTG 903
Db |||||
610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
QY 904 CTGGGGGCGCTCTTCTGCTGTGTACGCCACTACTCTTCTCATGATCGCAGAGCGGACCTG 963
Db |||||
630 LeuAlaGlyIlePheLeuCysTrrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
QY 964 GGGACCTGTTCTGCTCCGCGCATCTTCTTAGGGCTCGGCATGAGCATCAGCTACCGGCC 1023
Db |||||
650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
QY 1024 CTGCTGACCAAGACCAACCGGATTACCGCATCTTTTGGAGCGGCAACCGTGGTCACT 1083
Db |||||
670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
QY 1084 GCCCGCGCTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCCCTG 1143
Db |||||
690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709

Qy	1144	CAGCTGCTGGGCATCTCGGTGTGTGTTCGTGTGTGACCCCTCCCACTCGGTGGTGGCATTC	1203
Db	710	GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe	729
Qy	1204	CAGGACCAACGGACACTTGACCCCGCTTGGCCAGGGCGGTCTCAAGTGGAGCATCTCG	1263
Db	730	GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer	749
Qy	1264	GACCTGTCCCTCATCTGCTGCTGGGCTACAGCATGCTGCTGATGGTCAAGTGTACTGTG	1323
Db	750	AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal	769
Qy	1324	TACGCCATCAAGACCGGAGGCGTCCCGAGACCTTCAACGAGGCCAAGCCCATCGGCTTC	1383
Db	770	TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe	789
Qy	1384	ACCATGTACACCACTGCTGATTGTCTGGCTGGCCCTTCATCCCATCTTTTGGCACCTCA	1443
Db	790	ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer	809
Qy	1444	CAGTCAGCCGAACAGCTGTACATCCAGACAACACACTGACGGTCTCCGTGAGTCTGAGC	1503
Db	810	GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer	829
Qy	1504	GCTTCAGTGCCTGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTCTCCACCCG	1563
Db	830	AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro	849
Qy	1564	GAGCAGAACGTGCCCAACGCGCAGCTCTCAAGCCGTGTCTACCGCGCCACCATG	1623
Db	850	GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet	869
Qy	1624	TCCAAACAGTTCCACAGAAGGGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG	1683
Db	870	SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu	889
Qy	1684	TGTCAGAACCTGGAGACCCAGCGCTGGCTACCAAAACAGACCTACGTCACCTACCAAC	1743
Db	890	CysGlnAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn	909
Qy	1744	CATGCCATC	1752
Db	910	HisAlaIle	912

RESULT 5

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US-09-817-464-2
; Sequence 2, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-464-2

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Alignment Scores:				
Pred. No.:	9.63e-236	Length:	912	
Score:	3004.50	Matches:	564	
Percent Similarity:	97.77%	Conservative:	6	
Best Local Similarity:	96.74%	Mismatches:	12	
Query Match:	90.96%	Indels:	1	
DB:	4	Gaps:	1	
US-10-828-332-6 (1-1755) x US-09-817-464-2 (1-912)				
QY	7	GGGGTATCATCATCTTTGCCAACAGGATGACA--TCAGGGTTCCGACCGACTTCTCC	63	
DB	330	GlyAlaValThrLeuProGlyArgMetSerValArgGlyPheAspArgTyrPheSer	349	
QY	64	AGCCGACGCTGGACAAACAACAGGCGCAACTCTGTTTGGCGAGTTCTGGGAGACAAAC	123	
DB	350	SerArgThrLeuAaspAsnAargAsnIleTyrPheAlaGluPheTyrGluAspAsn	369	
QY	124	TTCCATTGCAAGTTAGCCGCCACCGCTCAAGAGGGAAGCCACATCAAGAAGTGCACC	183	
DB	370	PheHisCysLeuSerArgHisAlaLeuLysGlySerHisValLysLysCysThr	389	
QY	184	AACCGAGAGCCATCGGCGACACTCGCCTATGACGAGGAGGGAAGTGCAGTTCGTG	243	
DB	390	AsnArgGluArgIleGlyGlnAaspSerAlaTyrGluGlnGluGlyLysValGlnPheVal	409	
QY	244	ATTGACGCTGTGTACGCCATCGGCCACCGCTGCACGCATGCACCTGACCTGTGTGCC	303	
DB	410	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	429	
QY	304	GGCCGCTPAGCACTCTGCCCTCGCATGGACCCCGTGGATGGACCCAGCTGTTAAGTAC	363	
DB	430	GlyArgValGlyLeuCysProArgMetAaspProValAaspGlyThrGlnLeuLysTyr	449	
QY	364	ATCAGGAACGTCAACTTCTCAGGCATTCGCGGGAACCTGTAACTTCAATGAGAACCGA	423	
DB	450	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	469	
QY	424	GACGACCGGGCGCTACGACATCTACCAGTACCAACTGCCAATGGCTCGCGCCAGTAC	483	
DB	470	AspAlaProGlyAArgTyrAspIleTyrGlnTyrGlnLeuAArgAsnAspSerAlaGluTyr	489	
QY	484	AAGGTCATCGGCTCGTGACAGACCCTGCACCTCAGAAATAGACGGATGCAGTGGCCA	543	
DB	490	LysValIleGlySerTyrThrAspHisLeuHisLeuArgIleGluArgMetHisTyrPro	509	
QY	544	GGGAGTGGCCAGCAGCTCCCGCTCCATCTGCAGTCTGCCCTGCCACCGCGGAGCGGA	603	
DB	510	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	529	
QY	604	AAGAAGACTGTGAAGGGCATGGCTTGTCTGGCACTGCGAGCCCTGCACCGGTACACAG	663	
DB	530	LysLysThrValLysGlyMetProCysCysTyrPheLysCysGluProCysThrGlyTyrGln	549	
QY	664	TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATGCGGCCCCACAGAAC	723	
DB	550	TyrGlnValAaspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn	569	
QY	724	CGCAGAGCTCGCAGCCCATCCCCATTCGTCAAGTTGGATGGGACTCGCCGTGGGCCCTG	783	
DB	570	ArgThrGlyCysArgProIleProIleIleLysLeuGluTyrGlySerProTyrPheVal	589	
QY	784	CTGCCCTCTTCCTGGCGGTGGGCATCCCGCCACGCTGTTCTGGTGTGTACAGTTT	843	
DB	590	LeuProLeuPheLeuAlaValAGlyIleAlaAlaThrLeuPheValIleThrPhe	609	
QY	844	GTGGCTACAAACGATACCCCATCGTCAAGGCGCTCGGCCCGGGAACTGAGCTACGTGCTG	903	
DB	610	ValArgTyrAsnAaspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu	629	
QY	904	CTGGCGGCGATCTTTCTGTGCTACGCCACTACCTTCTCTCATGATCGCAGACCGGACCTG	963	
DB	630	LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu	649	

QY 964 GGGACCTGTTCTCGCTCGCGGCATCTTCTTAGGGCTCGGCATGAGCATGAGCTACCGGCC 1023
Db 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
QY 1024 CTGCTGACCAACCAACCGCATTTACCGCATCTTTGAGCGGCAACCGTCCGTCACT 1083
Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyArgSerValSer 689
QY 1084 GCCCGCGTTTCATCAGCGCGCCCTCGCAGCTGGCCATCACCTTCATCTCCCTG 1143
Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
QY 1144 CAGCTGCTCGGCATCTGCTGTGGTGTGGTGGGACCCCTCCACTCGGTGTGACTTC 1203
Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY 1204 CAGGACCAACGACACTTACCCCGCTTGGCCGGGCTGCTCAAGTGGACATCTCG 1263
Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
QY 1264 GACCTGTCCCTCATCTGCTGCTGGGTACAGCATGCTGCTGATGCTCACGTGTACTGTG 1323
Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TAGCCCATCAAGACCGGCGTGGCCGAGACCTTCAACGAGGCCAAGCCCATCGGCTTC 1383
Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACCATGTACACCACTGCATTTGCTGGCTGGCTTCATCCCTCATCTTTTGGCACTTCA 1443
Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
QY 1444 CAGTCAGCGCAACGCTGTACATTCAGACCAACCACTGACCGTCTCCGTGAGTCTGAGC 1503
Db 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
QY 1504 GCTTCAGTGTCTCGGGATGCTTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
QY 1564 GAGCAGACGTCGCCAAGCGCAGCGCAGTCTCAAGCGGTGGTCCACCGCCGACCATG 1623
Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
QY 1624 TCCAAACAGTTCCACACAGAGGCAACTTTCAGGCCCAATGGGAGGCCAAATCACAGCTG 1683
Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACCTGGAGACCCCGCTGCTACCAACAGACCTACCTCACCTTACACCAAC 1743
Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
QY 1744 CATGCCATC 1752
Db 910 HisAlaIle 912

RESULT 6

US-08-855-146-2

; Sequence 2, Application US/08855146

; Patent No. 6221609

; GENERAL INFORMATION:

; APPLICANT: Belagaje, Rama M.

; APPLICANT: Wu, Su

; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company

; STREET: Lilly Corporate Center/Patent Department

; CITY: Indianapolis

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/855,146

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/021,243

; FILING DATE: 07-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Webster, Thomas D.

; REGISTRATION NUMBER: 39,872

; REFERENCE/DOCKET NUMBER: X-10836

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (317) 276-6334

; TELEFAX: (317) 276-2764

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 908 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-855-146-2

Alignment Scores:

Pred. No.: 3,69e-184 Length: 908

Score: 2370.00 Matches: 437

Percent Similarity: 84.91% Conservative: 58

Best Local Similarity: 74.96% Mismatches: 86

Query Match: 71.75% Indels: 2

DB: 3 Gaps: 2

US-10-828-332-6 (1-1755) x US-08-855-146-2 (1-908)

QY 7 GGGGTATCATCATCTTTGCCAACGAGGATGACA---TCAGGGTTTCGACCGATACCTCTCC 63
Db 327 GlyAlaValThrIleLeuProLysArgAlaSerIleAspGlyPheAspArgTyrPheArg 346
QY 64 AGCGCGACGCTGGGCAACAACAGCGGCAACATCTGTTTGGCGAGTTCTGGGAGACAAC 123
Db 347 SerArgThrLeuAlaAsnAsnArgAsnValTrpPheAlaGluPheTrpGluGluAsn 366
QY 124 TTCCATTGCAAGTTGAGCGCGCCAGCGCTCAAGAGGGAAGCCACATCAAGAAGTGCAAC 183
Db 367 PheGlyCysLysLeuGlySerHisGly---LysArgAsnSerHisIleLysLysCysThr 385
QY 184 AACCGAGAGCGCATCGGCGAGGACTCGGCCTATGAGCAGGAGGGAAGGTGAGTTCTGTG 243
Db 386 GlyLeuGluArgIleAlaArgAspSerTyrGluGlnGluGlyLysValGlnPheVal 405
QY 244 ATTGACGCTGTGTACGGCCATGGCCGCTGACCGCTGACCGCTGACCGTGTGTGTCC 303
Db 406 IleAspAlaValTyrSerMetAlaTyrAlaLeuHisAsnMetHisLysAspLeuLysCysPro 425
QY 304 GCGCGCTAGGACTCTGCCCTCGCATGACCCCGTGGTGGTGGCCACCCAGCTCTTAAGTAC 363
Db 426 GlyTyrIleGlyLeuLysCysProArgMetSerThrIleAspGlyLysGluLeuGlyTyr 445
QY 364 ATCAGGAACGTCAACTTCTCAGGCATTCGCGGGGAACCTGTAACTTCAATGAGAACGGA 423
Db 446 IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly 465
QY 424 GACCGACCGGCGCTACGACATCTTACAGTACCAACTGCGCAATGGCTCGCGCCAGTAC 483
Db 466 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnIleThrAsnLysSerThrGluTyr 485
QY 484 AAGTTCATCGGCTGTGGAGACAGCACCTGACCTCAGAAATAGAGCGGATCGAGTGGCCA 543
Db 486 LysValIleGlyHisTrpThrAsnGlnLeuHisLysValGluAspMetGlnTrpAla 505

QY 544 GGGAGTGGCCAGCAGCTGCGGGTCCATCTGAGTCTGCCCTGCCAGCCGGGGAGCGA 603
Db HisArgGluHisThrHisProAlaSerValCysSerLeuProCysLysProGlyGluArg 525
QY 604 AAGAAAGCTGTGAAGGCAATGCTTGTCTGCGCACTGCGAGCCCTGCCACGGGTACCGAG 663
Db LysLysThrValLysGlyValProCysCysTrpHisCysGluArgCysGluGlyTyrAsn 545
QY 664 TACCAAGTGGACCGCTACACCTGTAAGACCTGCGCCCTACGACATGCGGCCCCACAGAGAAC 723
Db TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnMetAsn 565
QY 724 CGCAGAGCTGCCAGCCATCCCATCTCAAGTTGGAGTGGAGTCCGCTGGCGCGCTG 783
Db ArgThrGlyCysGlnLeuIleProLysLeuGluTrpHisSerProTrpAlaVal 585
QY 784 CTGCGCTCTCTCCGCGCTGGTGGCATCGCCGCGCAGCTGTGCTGGTGGTCACTGTTT 843
Db ValProValPheValAlaIleLeuGlyIleAlaThrPheValIleValThrPhe 605
QY 844 GTGGCTACACAGTACCCCATCGTCAAGCGCTCGGGCCGGGAACCTGACTAGTGTGCTG 903
Db ValArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeu 625
QY 904 CTGGCGGCGCTCTCTGCTGCTAGCCACTACCTCTCATGATCGCAGAGCCGGACCTG 963
Db LeuThrGlyIlePheLeuCysTyrSerIleThrPheLeuMetIleAlaAlaProAspThr 645
QY 964 GGGAGCTCTTCGCTCCGCGCATCTTCTCAGGGCTCGGCATGAGCATCAGCTACGCGGCC 1023
Db IleIleCysSerPheArgArgValPheLeuGlyLeuGlyMetCysPheSerTyrAlaAla 665
QY 1024 CTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAGAGGGGCAACGGTCTGGTCAGT 1083
Db LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysLysSerValThr 685
QY 1084 GCCCGCGTTTCATCAGCCGGCTCGCAGCTGGCCATCAGCTTCATCTCATCTCTCCTG 1143
Db AlaProLysPheIleSerProAlaSerGlnLeuValIleThrPheSerLeuIleSerVal 705
QY 1144 CAGTGTCTCGCATCTGCGTGTGGTTCGTGTGGACCCCTCCCATCGTGGTGGTGGACTTC 1203
Db GlnLeuLeuGlyValPheValTrpPheValValAspProProHisIleIleIleAspTyr 725
QY 1204 CAGGACCAACGGACACTTGTACCCCGCTTTGCGAGGGCGTCTCAAGTGGCACTCTCG 1263
Db GlyGluGlnArgThrLeuAspProGluLysAlaArgGlyValLeuLysCysAspIleSer 745
QY 1264 GACCTGTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGGTCCACGTCTACTGTG 1323
Db AspLeuSerLeuIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThrVal 765
QY 1324 TACGCCATCAAGACCCGAGGGCTGCCGAGACCTTCAACGAGGGCAAGCCCATCGGCTTC 1383
Db TyrAlaAsnLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 785
QY 1384 ACCATGTAACACCTGCAATGCTGTGGCTGCGCTTCATCCCACTCTTTTGGCACCTCA 1443
Db ThrMetTyrThrThrCysIleIleTrpLeuAlaPheIleProIlePheGlyThrAla 805
QY 1444 CAGTCAGCGGACAGCTGTACATCAGACACCAACCACTGACGGTCTCCGTGAGTCTGAGC 1503
Db GlnSerAlaGluLysMetTyrIleGlnThrThrThrLeuThrValSerMetSerLeuSer 825
QY 1504 GTTTCAGTGTCTCCGGGATGCTCTACATGCCAAAGTCTACATCATCTCTTCCACCCG 1563
Db AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHisPro 845
QY 1564 GAGCAGAACGTGCCCAAGCGCAAGCGCATGCTCAAGCGGTGGTCAACCGCCGCCCATG 1623
Db GluGlnAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThrMet 865

QY 1624 TCCAACAAGTTCCACAGAAAGGGCAACTTCAGGCCCAATGGGAAAGCCAAATCAGAGCTG 1683
Db 866 GlnSerLysLeuIleGlnLysGlyAsnAspArgProAsnGlyGluValLysSerGluLeu 885
QY 1684 TGTGAGAACTGGAGACCCCGAGCTGGCTACCAACAGACCTTACGTACCTACCAAC 1743
Db 886 CysGluSerLeuGluThrAsnThrSerSerThrLysThrThrTyrIleSerTyrSerAsn 905
QY 1744 CATGCCATC 1752
Db 906 HisSerIle 908
RESULT 7
US-08-823-110-1
; Sequence 1, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-823-110-1
Alignment Scores:
Pred. No.: 9,58e-181 Length: 908
Score: 2328.00 Matches: 430
Percent Similarity: 85.34% Conservative: 53
Best Local Similarity: 75.97% Mismatches: 81
Query Match: 70.48% Indels: 2
Gaps: 2
DB:
US-10-828-332-6 (1-1755) x US-08-823-110-1 (1-908)
QY 7 GGGGTATCATCATCTTTGCCAACGAGGATGACA---TCAGGGTTTCGACCCGATCTTCTCC 63

Db 327 GlyAlaValThrIleLeuProLysArgAlaSerIleAsePglyPheAspArgTyrPheArg 346
Qy 64 AGCCGACGCTGGACAAACAGCGGCAACATCTGGTTGGCCGAGTCTTGGGAGGACAAAC 123
Db 347 SerArgThrLeuAlaAsnAenArgAenValTrpPheAlaGluPheTrpGluGluAen 366
Qy 124 TTCCATTGCAAGTTGAGCGCCGACCGCTCAAGAGGGGAAGCCACATCAAGAAAGTGCACC 183
Db 367 PheGlyCysLeuLeuGlySerHisGly---LysArgAsnSerHisIleIleLysCysThr 385
Qy 184 AACCGAGAGCGCATCGGCGAGACTCGGCTATGAGCAGGAGGGAAGGTGAGTTCGTG 243
Db 386 GlyLeuGluArgIleAlaArgAspSerSerTyrGluGlnGluGlyLysValGlnPheVal 405
Qy 244 ATTGACGCTGTGTAGCCATGGCGGCGCTGCACCGCATCGACCTGACCTGTGTCCC 303
Db 406 IleAspAlaValTyrSerMetAlaTyrAlaLeuHiseAenMetHisLysAspLeuCysPro 425
Qy 304 GCGCGGTAGGACTCTGCGCTCGCATGAGACCCCGTGGATGGACCCAGCTGCTTAAGTAC 363
Db 426 GlyTyrIleGlyLeuCysProArgMetSerThrIleAspGlyLysGluLeuLeuGlyTyr 445
Qy 364 ATCAGGACGCTCAACTTTCAGGCATTCGCGGGAACCTGTAACTTCAATGAGAACGGA 423
Db 446 IleArgAlaValAsnPheAsnGlySerAlaGlyThrProValThrPheAsnGluAsnGly 465
Qy 424 GACGACCGCGGCGCTTACGACATCTACAGTACCACTCGCAATGGCTCGCGCCGAGTAC 483
Db 466 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnIleThrAsnLysSerThrGluTyr 485
Qy 484 AAGTCTATCGGCTGTGGACAGACCACTGCACCTCAGAAATAGCGGATGAGTGGCCA 543
Db 486 LysValIleGlyHisTrpThrAsnGlnLeuHiseLysLeuLysValGluAspMetGlnTrpAla 505
Qy 544 GGGAGTGGCCAGCAGCTCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCCTGCACCGGTACCAG 603
Db 506 HisArgGluHisThrHisProAlaSerValCysSerLeuProCysLysProGlyGluArg 525
Qy 604 AAGAAGACTGTGAAGGGATGCTTGTCTGGCACTGGAGCCCTGCACCGGTACCAG 663
Db 526 LysLysThrValLysGlyValProCysCysTrpHisCysGluArgCysGluGlyTyrAsn 545
Qy 664 TACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCTTACGACATCGCGCCCAACAGAAC 723
Db 546 TyrGlnValAspGluLeuSerCysGluLeuCysProLeuAspGlnArgProAsnMetAsn 565
Qy 724 CGCAGCAGTGCACGCCCATCCCATCGTCAAGTTGGAGTGGAGTCCGCGTGGCCGTG 783
Db 566 ArgThrGlyCysGlnLeuIleProIleIleLysLeuGluTrpHisSerProTrpAlaVal 585
Qy 784 CTGCCCTTCTCTCGCGGTGGTGGCATCGCGCCAGCTCTTCTGTGTGTGTGTCAGTTT 843
Db 586 ValProValPheValAlaIleLeuGlyIleIleAlaThrPheValIleValThrPhe 605
Qy 844 GTGCGCTACAAGTACCCCATCGTCAAGGCTCGCGCCGGAACCTGAGTACGTGCTG 903
Db 606 ValArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeu 625
Qy 904 CTGGCGGGCATTTCTGTGTACCCCATCTCTCTCATGATCGCAGAGCCGAGACCTG 963
Db 626 LeuThrGlyIlePheLeuCysTyrSerIleThrPheLeuMetIleAlaAlaProAspThr 645
Qy 964 GGGACCTGTCTCGCGCGCATCTTCTTAGGCTCGGCATGAGCATCAGCTACGCGGCC 1023
Db 646 IleIleCysSerPheArgArgValPheLeuGlyLeuGlyMetCysPheSerTyrAlaAla 665
Qy 1024 CTGCTGACCAACAGCAACCGATTACCGCATCTTTGAGCAGGGCAACCGTCCGTCACT 1083
Db 666 LeuLeuThrLysThrAsnArgIleHisArgIlePheGluGlnGlyLysLysSerValThr 685
Qy 1084 GCGCGCGCTTTCATCAGCGCGGCTCGCAGCTGGCCATCCTTCATCTCATCTCCCTG 1143

Db 686 AlaProLysPheIleSerProAlaSerGlnLeuValIleThrPheSerLeuIleSerVal 705
Qy 1144 CAGCTGCTCGGCATCTGCGTGTGGTTCGTGGTGGAGCCCTCCACTCGGTGGTGGACTTC 1203
Db 706 GlnLeuLeuGlyValPheValTrpPheValValAspProHisIleIleIleAspTyr 725
Qy 1204 CAGGACCAACGACACTTGACCCCGCTTGGCAGGGGGTGTCTCAAGTGGCAGCATCTCG 1263
Db 726 GlyGluGlnArgThrLeuAspProGluLysAlaArgGlyValLeuLysCysAspIleSer 745
Qy 1264 GACCTGTCCCTCATCTGCTGCTGGCTGACAGCATGCTGCTGCTACGCTGCTGCTG 1323
Db 746 AspLeuSerLeuIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThrVal 765
Qy 1324 TACGCCATCAAGACCCGAGGGCTGCCGAGACCTTCAACGAGGCCAAGCCCATCGGCTTC 1383
Db 766 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 785
Qy 1384 ACCATGTACACCACTGCTGCTGCTGGCTTCCCTCATCCCATCTTTTGGCACCTCA 1443
Db 786 ThrMetTyrThrThrCysIleIleTrpLeuAlaPheIleProIlePheGlyThrAla 805
Qy 1444 CAGTCAGCGGCAACAGCTGTACATCCAGAACACCACTGACGCTCTCGTGTAGTCTGAGC 1503
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Qy 1504 GCTTCAGTGTCCCTGGGATGCTTACATGCCCCAAAGTCTACATCATCTCTTCCACCCG 1563
Db 826 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHisPro 845
Qy 1564 GAGCAGAAGTGGCCCAAGCGGAGCGAGTCTCAAGCGGTGTCCACCGCCGCCACCATG 1623
Db 846 GluGlnAenValGlnLysArgLysArgSerPheLysAlaValThrAlaAlaThrMet 865
Qy 1624 TCCAAACAGTTTCAACAGAGGCAACTTTCAGGCCCAATGGGAGGCCAAATCAGAGCTG 1683
Db 866 GlnSerLysLeuIleGlnLysGlyAsnAspArgProAsnGlyGluValLysSerGluLeu 885
Qy 1684 TGTGAGAACCTGGAGACC 1701
Db 886 CysGluSerLeuGluThr 891
RESULT 8
US-08-604-298-1
; Sequence 1, Application US/08604298
; Patent No. 6084084
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hamerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,298
; FILING DATE: February 21, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

RESULT 9

Qy	541	CGAGGAGTGGCCAGCAGCTGCCCGGCTTCATCTGCGAGTCTGCCTCTCCACAGCCCGGGGAG	600
Db	512	GlyLysGlyValArgGluIleProSerSerValCysThrLeuProCysLysProGlyGln	531
Qy	601	CGAAGAAGACTGTGAAGGGGATGGCTTGCTGTGGCACTCGCAGCCCTGCACCGGGTAC	660
Db	532	ArgLysIysThrGlnLysGlyThrProCysCysTrpThrCysGluProCysAspGlyTyr	551
Qy	661	CAGTACCAAGTGGACCGCTACACTGTGAAGACCTGCCCTACGACATCGCGGCCACAGAG	720
Db	552	GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu	571
Qy	721	AACCGCAGGAGCTCCAGCCCATCCCATCGTCAAGTTGAGTGGAGTGGACTCGCGTGGCC	780
Db	572	AsnArgThrGlyCysGlnAsnIleProIleLysLeuGluTrpHisSerProTrpAla	591
Qy	781	GTGCTGCCCTCTTCTCCGTGGCGTGGTGGGATCGCCCGCACGCTGTTCTGGTGGTCA	840
Db	592	ValIleProValPheLeuAlaMetLeuGlyLysIleAlaThrIlePheValMetAlaThr	611
Qy	841	TTGTGTGGCTACAAAGATACCCCATCGTCAAGCCCTCGGCGCGGAACGTAGCTACGTG	900
Db	612	PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal	631
Qy	901	CTGCTGGCGGGCATCTTCTGTGTACGCCACACTACCTTCTCATGTATCGCAGAGCCGAC	960
Db	632	LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp	651
Qy	961	CTGGGACCTGTTCTCGCTCCGCGGCATCTCTTAGGGCTCGGCATGACATCAGCTACGCG	1020
Db	652	ValAlaValCysSerPheArgArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla	671
Qy	1021	GCCTGTGTACCAAGACCAACCGCATTTACCGCATTTTGAGCAGGCGCAACGGTGGCT	1080
Db	672	AlaLeuLeuThrIysThrAsnArgIleTyrArgIlePheGluGlnGlyLysSerVal	691
Qy	1081	AGTGCCCGCGTTCATCAGCCCGGCTCGCAGCTGGCCATCACCTTCATCTCTCATCTCC	1140
Db	692	ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer	711
Qy	1141	CTGCAGCTGCTCGGCATCTCGTGTGGTGTCTGTGTGAGACCCCTCCCATCGTGGTGGAC	1200
Db	712	ValGlnLeuLeuGlyValPheIleTrpPheGlyValAspProProAsnIleIleIleAsp	731
Qy	1201	TTCAGGACCAACGACACTGTGACCCCGGCTTTGCCAGGGCGGTGTCAAGTGCACATC	1260
Db	732	TyrAspGluHisIysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle	751
Qy	1261	TCGGACCTGTCCCTCATCTCGCTGTGGCTACAGCATGTGCTGTAGTGTCACTGTACT	1320
Db	752	ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr	771
Qy	1321	GTGTACGCCCATCAAGACCCGAGGCGTCCCGAGACCTTCAACAGGCGCAAGCCCATCGC	1380
Db	772	ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly	791
Qy	1381	TTCACCATGTACACCACTGATGTCTGTGGCTGTCCATTCGCCCATCTCTTTTGGCA	1440
Db	792	PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr	811
Qy	1441	TCACAGTCACCGCAAGCTGTACATCCAGACAACCACTGAGGGTCTCCGTGAGTCTG	1500
Db	812	AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu	831
Qy	1501	AGGCTTTCAGTGTCCCTGGGAGTCTCTACATGCCCCAAGTCTACATCATCTCTTCCAC	1560
Db	832	SerAlaSerValAlaLeuLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis	851
Qy	1561	CCGAGCAGAACGTGCCCAAGCGCAAGCGGAGTCTCAAGCGGTGTGTCAACGGCGCCAC	1620
Db	852	ProGluLeuAsnValGlnLysArgLysArgSerPheLysAlaValValThrAlaAlaThr	871

QY 1621 ATGTCCACACAGTTCACACAGAGAGGGCAACTTCAGGCCCAATGGGGNAGCCCAATCAGAG 1668
Db 872 MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 891
QY 1681 CTGTGTGAGAACCTGGAGACCCCAAGCGCTCGCTACCAACACAGAGCTACGTCACTACCTACACC 1740
Db 892 LeuCysGluAsnValAspProAsnSerProAlaAlaLysLysTyrValSerTyrAsn 911
QY 1741 AACCATGCCCATC 1752
Db 912 AsnLeuValIle 915

RESULT 13
US-08-176-401B-2
; Sequence 2, Application US/08176401B
; Patent No. 6274330
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176.401B
; FILING DATE: 30-DECEMBER-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-401B-2

Alignment Scores:
Pred. No.: 3,77e-171 Length: 915
Score: 2210.00 Matches: 406
Percent Similarity: 82.53% Conservative: 76
Best Local Similarity: 69.52% Mismatches: 100
Query Match: 66.91% Indels: 2
DB: 3 Gaps: 2

US-10-828-332-6 (1-1755) x US-08-176-401B-2 (1-915)

QY	7	GGGGTATCATCATCTTTGCCCAAGAGATGACA----	TCAGGGTTCCAGCGATACTTCTCC	63
DB	332	GlyAlaLeuThrLeuGlnProLysArgAlaThrValGluGlyPheAspAlaIyrPheThr		351
QY	64	AGCCGCACGCTGGACAAACACACAGGCGCAACATCTCGTTTCCGAGTTCTGGGAGGACAAAC	123	
DB	352	SerArgThrLeuGluGluAsnArgAsnValTyrPheAlaGluIyrTrpGluGluAsn	371	

Qy	124	TTCCATTGCGAAGTTGAGCGCCACGCGCTCAAGAAAGGAAGCCACATCAAGAAAGTGCACC	183
Db	372	PhaAsnCysIysLeuThrIleSerGlySerIysGluAspThrAspAraGlyCysThr	391
Qy	184	AACCGAGCGCATCGGACGAGTCTCGGCTATGACGACGAGGAGGAGTGCAGTTCGTG	243
Db	392	GlyGlnGluArgIleGlyLysAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal	411
Qy	244	ATTGACCGCTGTAGCGCATGGGCGACGCGCTGCACGCCCATGACACCGCTGTGTCCC	303
Db	412	IleAspAlaValTyrAlaMetAlaHisAlaLeuHisIleMetAsnLysAspLeuCysAla	431
Qy	304	GGCCGCTAGGACTCTCCCTCGCATGGACCCCGCTGGATGCACCCAGCTGCTTAAGTAC	363
Db	432	AspTyrArgGlyValCysProGluMetGluGlnAlaGlyGlyLysLysLeuLeuLysTyr	451
Qy	364	ATCAGGAACGTCAACTTCTCAGGCATTGCGGGGACCCCTGTAACTTTCATAGAACGGA	423
Db	452	IleArgHisValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly	471
Qy	424	GACCCACCGGGCGCTACGACATCTACGAGTACCACCTACGCGCAAT---GGCTCGCCGAG	480
Db	472	AspAlaProGlyAlaTyrAspIlePheGlnTyrGlnThrThrAsnThrThrAsnProGly	491
Qy	481	TACAAGTCTATCGGCTCGTGGACAGACCACTGCACCTCAAGATAGACGGATGCAGTGG	540
Db	492	TyrArgLeuIleGlyGlnTyrThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTyr	511
Qy	541	CCAGGGAGTGGCAGAGCTGCGCGCTCCATCTGCAGTCTGCCCTGCCAGCCGCGGAG	600
Db	512	GlyLysGlyValArgGluIleProSerSerValCysThrLeuProCysLysProGlyGln	531
Qy	601	CGAAGAAGACTGTGAAGGGCATGGCTTGCTGCGCACTGCAGCGCCCTGCACCGGGTAC	660
Db	532	ArgLysLysThrGlnLysGlyThrProCysCysTyrThrCysGluProCysAspGlyTyr	551
Qy	661	CAGTACCAAGTGGACCGCTACACTGTAAGACCTGCCCTACGACATCGCGGCCACAGAG	720
Db	552	GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnAraGProAsnGlu	571
Qy	721	AACCGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGAGTGGAGTGCCTGCCGTGGGCC	780
Db	572	AsnArgThrGlyCysGlnAsnIleProIleIleLysLeuGlnTyrHisSerProTyrAla	591
Qy	781	GTGCTGCCCTCTTCCTGGCGCTGGTGGGATCGCCGCGCTGTTGCTGGTGGTCAAG	840
Db	592	ValIleProValPheLeuAlaMetCLeuGlyIleIleAlaThrIlePheValMetAlaThr	611
Qy	841	TTTGTGCGCTACAAACGATACCCCATCGTCAAGCGCTCGGCGCGGAACTGAGCTACGTG	900
Db	612	PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal	631
Qy	901	CTGCTGCGGGGCACTTTCTGTGTACGCCACTACCTTCCTCATGATCGCAGAGCCGGAC	960
Db	632	LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp	651
Qy	961	CTGGGGACCTGTTGCTCGCGCATCTTCTTAGGGCTCGGCATGACATCAGTACGCG	1020
Db	652	ValAlaValCysSerPheAraGArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla	671
Qy	1021	GCCCTGTGCACAGACCAACCGCATTTACCGCATCTTTGACGAGGAGCAACCGTCCGTC	1080
Db	672	AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysLysSerVal	691
Qy	1081	AGTCCCGGGTTCATCAGCCCGGCTCGGAGCTGGCGCATCAGCTTCATCTCATCTCC	1140
Db	692	ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer	711
Qy	1141	CTGCAGCTGCTCGCATCTCGTGTGTGTTGCTGGTGGACCCCTCCCATCGTGGTGGAC	1200
Db	712	ValGlnLeuLeuGlyValPheIleTyrPheGlyValAspProProAsnIleIleIleAsp	731
Qy	1201	TTCCAGGACCAACGGACACTTGACCCCGCTTTTCCACAGGGCGGTGCTCAAGTGCACATC	1260

Db	732	TyrAspGluHisLysThrMetAsnProGluGlnAlaAArgGlyValLeuLysCysAspIle	751
QY	1261	TCGGACCTGTCCTCATCTGCCTGCTGGGCTACAGCATCTGCTGATGGTTCAGCTGTACT	1320
Db	752	ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr	771
QY	1321	GTGTAGCCCATCAAGACCCGAGGCGTGCCTTCAACAGAGGCCAAGCCCATCGGC	1380
Db	772	ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly	791
QY	1381	TTTCACCATGTATACACCATGCTGCTGGCTGGCTTCATCCCATCTTTTGGSCACC	1440
Db	792	PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThr	811
QY	1441	TCACAGTCAGCCGACCAAGCTGTACATCCAGACAACACACTGACGGTCTCCGTGAGTCTG	1500
Db	812	AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrLeuThrIleSerMetAsnLeu	831
QY	1501	AGGCTTTCAGTTCCTCGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCAC	1560
Db	832	SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIleIlePheHis	851
QY	1561	CGGAGCAGAACTGTCGCCCAAGCGCAGCGCAGTCTCAAAGCCGTGTACACGCCGCCACC	1620
Db	852	ProGluLeuAsnValGlnLysArgLysAspSerPheLysAlaValValThrAlaAlaThr	871
QY	1621	ATGTCCAAACAGTTTCACAGAAAGGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAG	1680
Db	872	MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu	891
QY	1681	CTGTGTGAGAACTGTGAGACCCCGCGCTGCTACCAACAGACCTACGTCACTACACACC	1740
Db	892	LeuCysGluAsnValAsnProAsnSerProAlaAlaLysLysLysTyrValSerTyrAsn	911
QY	1741	AACCATGCCATC	1752
Db	912	AsnLeuValIle	915

RESULT 14

PCT-US94-14989-2

; Sequence 2. Application PC/TUS9414989

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS

; NUMBER OF SEQUENCES: 3

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/14989

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/176,401

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCE/DOCKET NUMBER: 13952-18PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 467-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 915 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-14989-2


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; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-4

Alignment Scores:
Pred. No.: 1 186-169 Length: 867
Score: 2191.50 Matches: 405
Percent Similarity: 81.85% Conservative: 73
Best Local Similarity: 69.35% Mismatches: 99
Query Match: 66.35% Indels: 7
DB: 3 Gaps: 3

US-10-828-332-6 (1-1755) x US-08-617-785-4 (1-867)
QY 7 GGGGTATCATCTTTGCCAACGAGGATGACA---TCAGGGTTCCGACCGGATCTCTCC 63
DB 277 GlyAlaIleThrIleGlnProLysArgAlaThrValGluGlyPheAspAlaTyrPheThr 296
QY 64 AGCCGACGCTGGACAAACAGCGGCAACATCTGTTTGGCGAGTCTGGGAGCAAC 123
DB 297 SerArgThrLeuGluAsnAsnArgAsnValTyrPheAlaGluTyrTrpGluGluAsn 316
QY 124 TTCCATTCCAGTTGACGCGGCACCGCTCAAGAGGGAAGCCACATCAAGAGTGCAC 183
DB 317 PheAsnCysLysLeuThrIleSerGlySerLysLysGluAspThrAspArgLysCysThr 336
QY 184 AACCCAGAGCGCATCGGCGAGCTCGCCCTATGAGCAGGAGGGAAGCTGCAGTTCGTG 243
DB 337 GlyGlnGluArgIleGlyAspSerAsnTyrGluGlnGluGlyLysValGlnPheVal 356
QY 244 ATTGACGTGTGTACGCCATGGGCGACCGCTGACGCGCATGACCGCTGCTGTGTC 303
DB 357 IleAspAlaValTyrAlaMetAlaHisAlaLeuHisHisMetAsnLysAspLeuCysAla 376
QY 304 GGCCGCTAGACTCTGCTCGCATGACCCCGTGGATGTCACCCAGCTCTTAAGTAC 363
DB 377 AspTyrArgGlyValCysProGluMetGluGlnAlaGlyGlyLysLeuLeuLysTyr 396
QY 364 ATCAGGAACGTCAACTTCTCAGGCAATTCGGGGAAACCTGTAACTTCAATGAGAACGGA 423
DB 397 IleArgAsnValAsnPheAsnGlySerAlaGlyThrProValMetPheAsnLysAsnGly 416
QY 424 GACGACCGGGCGCTACGACATCTACAGTACCAACTGCGCAATGGCTCG---GCCGAG 480
DB 417 AspAlaProGlyArgTyrAspIlePheGlnTyrGlnThrThrAsnThrSerAsnProGly 436
QY 481 TACAGGTTCATCGGCTCTGGACAGACACCTGACCTCAGAAATAGACCGGATGACGTGG 540
DB 437 TyrArgLeuIleGlyGlnTrpThrAspGluLeuGlnLeuAsnIleGluAspMetGlnTrp 456
QY 541 CCAGGGAGTGGCGACAGCTCGCGGCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 457 GlyLysGlyValArgGluIleProLysValCysThrLeuProCysLysProGlyGln 476
QY 601 CGAAAGAACTGTGAAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 477 ArgLysThrGlnLysGlyThrProCysCysTyrThrCysGluProCysAspGlyTyr 496
QY 661 CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 497 GlnTyrGlnPheAspGluMetThrCysGlnHisCysProTyrAspGlnArgProAsnGlu 516
QY 721 AACCCAGCGAGTGGCGACCGCATCCCATCGTCAAGTTGGAGTGGGACTCGCGCTGGGCCC 780
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Db 517 AsnArgThrGlyCysGlnAspIleProIleIleLysLeuGluTrpHisSerProTrpAla 536
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DB 537 ValIleProValPheLeuAlaMetLeuGlyIleIleAlaThrIlePheValMetAlaThr 556
QY 841 TTTGTGGCTTACCAACGATACCCCATCGTCAAGGCTTCGGGCGCGGGAACCTAGCTAGTGTG 900
DB 557 PheIleArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrVal 576
QY 901 CTGCTGGCGGCGATCTTTCTGTGTACGCCATCTTCTGATGCTGATGCTGATGCTGATGCTG 960
DB 577 LeuLeuThrGlyIlePheLeuCysTyrIleIleThrPheLeuMetIleAlaLysProAsp 596
QY 961 CTGGGGACCTGTTGCTCCGCGCATCTTCTAGGCTCGGCATCGGCATCGCATCGATCGCG 1020
DB 597 ValAlaValCysSerPheArgValPheLeuGlyLeuGlyMetCysIleSerTyrAla 616
QY 1021 GCCCTGTGTACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGCGCAACGCTCGGTC 1080
DB 617 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysSerVal 636
QY 1081 AGTCCCCCGGCTTTCATCAGCCCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC 1140
DB 637 ThrAlaProArgLeuIleSerProThrSerGlnLeuAlaIleThrSerSerLeuIleSer 656
QY 1141 CTGCGAGTGTCTCGGCATCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 657 ValGlnLeuLeuGlyValPheIleTyrPheGlyValAspProProAsnIleIleAsp 676
QY 1201 TTCCAGGACCAACCGCACCTTGACCCCGCTTTCAGGCGCGCTGCTCAAGTGGGACATC 1260
DB 677 TyrAspGluHisLysThrMetAsnProGluGlnAlaArgGlyValLeuLysCysAspIle 696
QY 1261 TCGGACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 697 ThrAspLeuGlnIleIleCysSerLeuGlyTyrSerIleLeuLeuMetValThrCysThr 716
QY 1321 GTGTACCCCATCAAGACCCGCGGCTGCCGAGACCTTCAACGAGGCGCAACCCATCGGC 1380
DB 717 ValTyrAlaIleLysThrArgGlyValProGluAsnPheAsnGluAlaLysProIleGly 736
QY 1381 TTCAACCATGACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 737 PheThrMetTyrThrThrCysIleValTyrPheAlaPheIleProIlePheGlyThr 756
QY 1441 TCACAGTCAGCGCAAGCTGTACATCAGAACACCACTGACGCTGCTGCTGCTGCTGCTGCTG 1500
DB 757 AlaGlnSerAlaGluLysLeuTyrIleGlnThrThrThrLeuThrIleSerMetAsnLeu 776
QY 1501 AGCGCTTCAGTGTCCCTGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCAC 1560
DB 777 SerAlaSerValAlaLeuGlyMetLeuTyrMetProLysValTyrIleIlePheHis 796
QY 1561 CCGGAGCAGACGTCGCCAAGCGCAGCTCTCAAGCGCTGCTCAAGCGCTGCTGCTGCTGCTGCTG 1620
DB 797 ProGluLeuAsnValGlnLysArgLysSerPheLysAlaValValThrAlaAlaThr 816
QY 1621 ATGTCCAACAGTTCACAGAGGCAACTTACGCGCCCAATGCGGAGCGCAATACAG 1680
DB 817 MetSerSerArgLeuSerHisLysProSerAspArgProAsnGlyGluAlaLysThrGlu 836
QY 1681 CTGTGTGAGAACCTGGAG-----ACCCAGCGCTGGCTTACCACAAACAGACC 1725
DB 837 LeuCysGluAsnValAspProAsnAsnCysIleProProValArgLysSerValGlnLys 856
QY 1726 TACGTACCTAC 1737
DB 857 SerValThrTrp 860
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Search completed: June 17, 2005, 18:55:27
Job time : 111 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 17, 2005, 18:18:26 ; Search time 254 Seconds

(without alignments)
5344.602 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 3303

Sequence: 1 atgcagggggtatcatc.....acaccaaccatgccatctag 1755

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/US10828332/tunat_17062005_171335_24935/app_query.fasta_1.1927
-DB=A_Genesec -OFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOPEXT=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10828332 @CGN 1 1 272 @runat 17062005 171335 24935 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES @WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Genesecp_16Dec04:*
1: Genesecp1980s:*
2: Genesecp1990s:*
3: Genesecp2000s:*
4: Genesecp2001s:*
5: Genesecp2002s:*
6: Genesecp2003as:*
7: Genesecp2003bs:*
8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3107	94.1	584	6	ABR56244 Rat gluta
2	3050.5	92.4	604	6	ABG74133 Rat metab
3	3050.5	92.4	912	7	ADES8164 Rat Prote
4	3050.5	92.4	912	7	ADES8168 Rat Prote
5	3017	91.3	909	8	ADO29095 Mouse nov
6	3004.5	91.0	909	5	AAO15101 Human ph8
7	3004.5	91.0	912	2	AAR82658 Human mgl
8	3004.5	91.0	912	5	AAR23757 Human met
9	3004.5	91.0	912	6	ABP81846 Human met
10	3004.5	91.0	912	7	ABE58170 Human Pro

11	3004.5	91.0	912	7	ADE58166	Ades58166 Human Pro
12	3004.5	91.0	912	8	ADO29094	Ado29094 Human nov
13	3004.5	91.0	912	8	ADQ89114	Adq89114 Human uro
14	3001.5	90.9	912	2	AAR72092	Aar72092 Human mgl
15	2912.5	88.2	591	8	ADR08623	Adr08623 Human pro
16	2852.5	86.4	886	8	ABM84666	Abm84666 Human dia
17	2752.5	83.3	796	8	ADR10452	Adr10452 Human pro
18	2752	83.3	862	8	ABM84667	Abm84667 Human dia
19	2711	82.1	1422	5	AAO15102	Aao15102 Human phm
20	2377	72.0	908	6	ABR62488	AbR62488 Human met
21	2377	72.0	908	8	ABR62489	AbR62489 Human met
22	2377	72.0	908	8	ADO29476	Ado29476 Human GPC
23	2374	71.9	908	6	ABR62490	AbR62490 Human met
24	2370	71.8	908	2	AAW41568	Aaw41568 Human met
25	2370	71.8	908	5	ABO95964	AbO95964 Human GRM
26	2370	71.8	908	6	ABP81850	Abp81850 Human met
27	2370	71.8	908	7	ADE31729	AdE31729 Human 255
28	2370	71.8	908	8	ADO89128	AdO89128 Human uro
29	2369	71.7	908	6	ABR62491	AbR62491 Human met
30	2348	71.1	1142	4	ABG29451	Abg29451 Novel hum
31	2336	70.7	908	8	ADO29477	Ado29477 Mouse GPC
32	2328	70.5	908	2	AAW49928	Aaw49928 Human met.
33	2328	70.5	913	4	ABG29452	Abg29452 Novel hum
34	2319	67.2	915	5	ABG95155	Abg95155 Human GPC
35	2319	67.2	915	6	ABP81849	Abp81849 Human met
36	2219	67.2	915	7	ADE55969	AdE55969 Human Pro
37	2219	67.2	915	7	ADJ93191	Adj93191 Human met
38	2219	67.2	915	8	ADO29103	Ado29103 Human nov
39	2215	67.1	915	2	AAR72097	Aar72097 Human mgl
40	2214	67.0	915	5	ABG95164	Abg95164 Human GPC
41	2214	67.0	915	8	ADO29104	Ado29104 Mouse nov
42	2213	67.0	915	5	ABG95165	Abg95165 Human GPC
43	2212	67.0	915	5	ABG95166	Abg95166 Human GPC
44	2210	66.9	915	2	AAR80479	Aar80479 Rat metab
45	2210	66.9	915	6	AAE30199	Aae30199 Rat metab

ALIGNMENTS

RESULT 1

ABR56244

ID ABR56244 standard; protein; 584 AA.

XX

AC ABR56244;

XX

DT 20-NOV-2003 (first entry)

XX

DE Rat glutamic acid receptor.

XX

Rat; anorectic; antiulcer; antidiabetic; laxative; antidiarrheic;

glutamic acid receptor; receptor; gastrointestinal tract disorder;

sitiefagia; obesity; ulcer; diabetes; constipation; diarrhoea.

XX

OS Rattus norvegicus.

XX

PN WO2003035873-A1.

XX

PD 01-MAY-2003.

XX

PF 23-OCT-2002; 2002WO-JP010984.

XX

PR 23-OCT-2001; 2001JP-00325159.

XX

(AJIN) AJINOMOTO CO INC.

San Gabriel A, Maekawa T, Uneyama H, Torii K;

WPI; 2003-430418/40.

N-PSDB; ACC70676.

XX

Novel glutamic acid receptor protein and encoded DNA, applicable in screening agonists or antagonists of glutamic acid or allosteric modulator for use as drugs in ameliorating symptoms and diseases e.g.

PT obesity.
 XX Claim 3; Page 33-35; 39pp; Japanese.
 XX The present sequence is the protein sequence for rat glutamic acid receptor. The receptor has a transmembrane domain and an intracellular domain common to type 4 metabotropic glutamic acid receptor protein, and an extracellular domain shorter by 316 or 327 amino acid residues than type 4 metabotropic glutamic acid receptor protein. The receptor and its coding sequence are useful in screening agonists or antagonists of glutamic acid or allosteric modulator for use as drugs in ameliorating symptoms and diseases due to abnormal metabolism in gastrointestinal tract including small and large intestines e.g. sititiegria, obesity, ulcer, diabetes, constipation and diarrhoea

XX SQ Sequence 584 AA;

Alignment Scores:

Pred. No.:	9,04e-217	Length:	584
Score:	3107.00	Matches:	584
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.07%	Indels:	0
DB:	6	Gaps:	0

US-10-828-332-6 (1-1755) x ABR56244 (1-584)

QY 1 ATGCGAGGGTATCATCTTTGCAAGAGATGACATCAGGTTTCAGCGATATTC 60
 DB 1 MetProGlyValSerSerLeuProThrArgMetThrSerGlyPheAspArgTyrPhe 20

QY 61 TCCAGCCGACCTGGACACACAGCGCACATCTGGTTGCGAGTCTCTGGGAGGAC 120
 DB 21 SerSerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAsp 40

QY 121 AACTTCCATTGCAAGTTGAGCGCCACCGCTCAAGAGGAGGCCACATCAAGAAGTGC 180
 DB 41 AsnPheHisCysLeuLeuSerArgHisAlaLeuLeuLysLysGlySerHisIleLysLysCys 60

QY 181 ACCAACGAGAGCGCATCGGAGGACTCGGCTATGAGCAGGAGGGGAAAGTGCAGTTC 240
 DB 61 ThrAsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPhe 80

QY 241 GTGATTGAGCTGTGTACCCATGGCCGACGCGCTGACGCGCATCCAGCGTGACCTGTGT 300
 DB 81 ValIleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCys 100

QY 301 CCGCGCGCGTAGGACTCTGCCCTCGCATGGACCCCGTGGATGGACCCAGCTGCTTAAG 360
 DB 101 ProGlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLys 120

QY 361 TCATCAGGAACGTCACCTTCTCAGGATTTGGGGAAACCCCTGTAACTTCAATGAGAAC 420
 DB 121 TyrIleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsn 140

QY 421 GGAGAGCGACCGGGGCTTACACATCTACAGTACCACTGCGCAATGGCTCGGCCGAG 480
 DB 141 GlyAspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGlu 160

QY 481 TACAAAGTTCATCGGTCGTGGACAGACACCTGCACCTCAGAAATAGAGCGAGTGG 540
 DB 161 TyrLysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetGlnTrp 180

QY 541 CCAGGAGTGGCAGCAGCTCGCGCTCCATCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 181 ProGlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGlu 200

QY 601 CCAAGAGACTGTGAGGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 201 ArgLysLysThrValLysGlyMetAlaCysCysTrpHisCysGluProCysThrGlyTyr 220

QY 661 CAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCGCCCTACGACATCGCGCCACAGAG 720

DB 221 GlnTyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGlu 240
 QY 721 AACCGCAGAGCTGCGCAGCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCCTGGGCC 780
 DB 241 AsnArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAla 260
 QY 781 GTGCTGCCCTCTCTCTGGCGGTGGTGGATCCCGCCACGCTGTTCTGTCGTGGTGCACG 840
 DB 261 ValLeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValThr 280
 QY 841 TTTGTGCGCTACACAGATACCCCATCGTCAAGCCCTCGGCGCGGAACTAGTACGTG 900
 DB 281 PheValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrVal 300
 QY 901 CTGCTGGGGGCGATCTTCTGTGTAGCCACCTACCTTCTCATGATCGGAGCCGCGAC 960
 DB 301 LeuLeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAsp 320
 QY 961 CTGGGAGACCTGTTCTGCTCCGCGCATCTTCTAGGCTCGGCATGAGCATCAGTACGCG 1020
 DB 321 LeuGlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAla 340
 QY 1021 GCCCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGAGGAAACGTCG 1080
 DB 341 AlaLeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerVal 360
 QY 1081 AGTCCCGCGGTTTTCATCAGCCGCGCTCGCAGCTGGCCATCACCTTCATCTCATCTCC 1140
 DB 361 SerAlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheIleLeuIleSer 380
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 DB 381 LeuGlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAsp 400
 QY 1201 TTCAGAGACCAACGACACATTGACCCCGCTTTCAGGCGGCTGCTCAAGTGCAGCATC 1260
 DB 401 PheGlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIle 420
 QY 1261 TCGACCTGTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 DB 421 SerAspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThr 440
 QY 1321 GTGTACCGCATCAAGACCCGAGCGGTGCCGAGACCTTCAACGAGGCGCAAGCCCATCGGC 1380
 DB 441 ValTyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGly 460
 QY 1381 TTCACCATGTACACCATCTGCATTGTCTGGCTGGCTTTCATCCCATCTTTTGGCACC 1440
 DB 461 PheThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThr 480
 QY 1441 TCACAGTCACGCGACAGCTGTACATCCAGACACACACTGACGCTCCCGTCCGTCAGTCTG 1500
 DB 481 SerGlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeu 500
 QY 1501 AGCGCTTCAGTGTCCCTGGGGATCTCTACATGCCCCAAAGCTTACATCATCTCTTCCAC 1560
 DB 501 SerAlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHis 520
 QY 1561 CCGGAGCAGAACGTGCCCAAGCGCAAGCGAGTCTCAAAGCGGTGTCACCGCGCCAC 1620
 DB 521 ProGluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThr 540
 QY 1621 ATGTCCCAACAGTTTCACAGAGGCGCACTTCAGGCGCCATGGGAGCCAAATCAGAG 1680
 DB 541 MetSerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGlu 560
 QY 1681 CTGTGTGAGAACCTGGAGACCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
 DB 561 LeuCysGluLeuLeuGluThrProAlaLeuAlaThrLysGlnThrThrValThrThr 580
 QY 1741 AACCATGCCATC 1752
 DB 581 AsnHisAlaIle 584

expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/published/bct/sequences](http://wipo.int/pub/published/bct/sequences).

Sequence 912 AA;

Alignment Scores:	1,298-212	Length:	912
Pred. No.:	Score:	Matches:	575
	3050.50	Conservative:	2
Percent Similarity:	98.97%	Mismatches:	5
Best Local Similarity:	98.63%	Indels:	1
Query Match:	92.36%	Gaps:	1
DB:	7		

US-10-828-332-6 (1-1755) x ADE58168 (1-912)

Qy	7	GGGGTATCATCATCTTGGCAACGAGGATGACA---TCAGGGTTCGACCGCATCTCTCC	63
Db	330	GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer	349
Qy	64	AGCGCAGCGTCGACAACAACAGGGCGCAACATCTGGTTTGCAGAGTCTCGGAGGACAAC	123
Db	350	SerArgThrLeuAspAsnAsnArgArgAsnIleTyrPheAlaGluPheTyrGluAspAsn	369
Qy	124	TTCATTGCAAGTTGAGCGCGCCACCGCTCTAAGAAGGGAAGCCACATCAAGAAGTGCACC	183
Db	370	PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisIleLysLysCysThr	389
Qy	184	AACCGAGAGCGCATCGGCAGGACATCGCGCTTACGACGAGGAGGAGGTCAGTTCTCGTG	243
Db	390	AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal	409
Qy	244	ATTGACGCTGTGTAGCCATGCGGCACCGCGCTGCACGCCATGCACCGCTGCCTGTCTCC	303
Db	410	IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro	429
Qy	304	GGCGCGTATAGGACTCTGCGCTCGCATGGAACCGCTGGATGGCACCCAGCTGTTAGTAC	363
Db	430	GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr	449
Qy	364	ATCAGGAACGTCAACTTCTCAGGCATTGCGGGGAACCTGTAACTTCAATGAGAAGCGGA	423
Db	450	IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly	469
Qy	424	GAGCACCGGGCGCTACGACATCTACCACTACCACTGCGCAATGCTCGCGCGAGTAC	483
Db	470	AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnGlySerAlaGluTyr	489
Qy	484	AAGGTATCGGCTCGTGGACAGACACCTGCACCTCAGAAATAGACGGATGCGAGTGC	543
Db	490	LysValIleGlySerTrpThrAspHisIleuHisIleuArgIleGluArgMetGlnTyrPro	509
Qy	544	GGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCTGCGCTGCCAGCCCGGGAGCGGA	603
Db	510	GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg	529
Qy	604	AAGAAGACTGTGAAGGGCATGCTTGTCTGGCATGTCGAGCCCTGCACCGGTTACCAG	663
Db	530	LysLysThrValIysGlyMetAlaCysCysTrpHisCysGluProCysTrpGlyTyrGln	549

|||||
910 HisAlaIle 912

Db
RESULT 5
ADO29095 standard; protein; 909 AA.

Xc ADO29095;
XX DT 29-JUL-2004 (first entry)
Xx DE Mouse novel GPCR GRM4, SEQ ID NO:194.

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
transgenic mouse; neurological disorder; adrenal gland disorder;
colon disorder; intestinal disorder; cardiovascular disease;
muscular disorder; blood disorder; immune disorder; bone disorder;
joint disorder; metabolic disorder; nutritive disorder; cancer;
kidney disorder; liver disorder; lung disorder; breast disorder;
ovary disorder; uterus disorder; prostate disorder; testis disorder;
skin disorder; stomach disorder; pancreas disorder; spleen disorder;
thyroid disorder; thyroid disorder; antiparkinsonian; antimanic;
cytostatic; antiinflammatory; vasotropic; angiogenic; antiarrhythmic;
CNS; central nervous system; respiratory; antididiarrhoic; antidiabetic;
viralicide; hepatotrophic; antibacterial; antianaemic; antiseborrhoeic;
dermatological; antiulcer; antithyroid; antiallergic; anorectic;
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
murine; receptor.

KW Mus musculus.
OS WO2004040000-A2.
XX PD 13-MAY-2004.
XX PF 09-SEP-2003; 2003WO-US028226.
XX PR 09-SEP-2002; 2002US-0409303P.
XX PT 09-APR-2003; 2003US-0461329P.
XX PA (PRIM-) PRIMAL INC.
XX PI Gaitanaris GA, Bergmann JE, Gragorov A, Hohmann J, Li F,
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
DR WPI: 2004-390329/36.
DR N-PSDB; ADO29096.

XX Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
XX PS Claim 1; SEQ ID NO 194; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds comprising a GPCR gene of the invention; a transgenic mouse mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice, kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel

```
QY 724 CGCAGAGCTGCAGCCCATCCCATCTCAAGTTGGAGTGGACTCGCGTGGCGCTG 783
Db 567 ArgThrSerCysGlnProIleProIleValLysLeuGluTrpAspSerProTrpAlaVal 586
QY 784 CTGCGCCCTCTTCTCGCGCTGGTGGCATCGCGCAGCGTGTTCGTGGTGGTCACTGTT 843
Db 587 LeuProLeuPheLeuAlaValValGlyIleAlaIleThrLeuPheValValThrPhe 606
QY 844 GTGCGCTCAACAGATACCCCATCTCAAGGCTTCGGCCCGGAACTGAGCTACGTGCTG 903
Db 607 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 626
QY 904 CTGGCGGCGATCTTCTGTGCTACCGCATCTACCTCTCTCATGATCGCAGCGGACCTG 963
Db 627 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 646
QY 964 GGGACCTGTTCTCGCTCGCGCATCTTCTAGGCTTCGGCATGAGCATCAGCTACGCGGCC 1023
Db 647 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 666
QY 1024 CTGCTGACCAAGACCAACCGCATTTACCGCATCTTGTAGAGCGGCAAAACGGTGGTCACT 1083
Db 667 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 686
QY 1084 GCCCGCGCTTTCATGAGCCGCGCTCGAGCTGGCGCATCCTTCATCTCTCTCCCTG 1143
Db 687 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheValIleSerLeu 706
QY 1144 CAGCTGCTCGGATCTGCGTGGTTCGTGGAGCCCTCCCATCTCGTGGTGGACTTC 1203
Db 707 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 726
QY 1204 CAGGACCAACGACACTTGACCCCGCTTTCAGGCGGTGCTCAAGTGGACATCTCG 1263
Db 727 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 746
QY 1264 GACCTGCTCCTCATCTGCTGCTGGCTACAGCATGCTGCTGATGGTCACGTGACTGTG 1323
Db 747 AspLeuSerLeuIleCysLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 766
QY 1324 TACGCGCATCAAGACCGAGCGCTGCCGAGACTTCAACGAGGCCCAAGCCATCGGCTTC 1383
Db 767 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 786
QY 1384 ACCATGTACACACTGCACTGCTGCTGGCTGCTTCATCCCATCTTTTGGCACCTCA 1443
Db 787 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 806
QY 1444 CAGTCAGCGCAGACTGTACATCCAGACCAACCACTGACGCTCTCGTGGTGTGAGC 1503
Db 807 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 826
QY 1504 GCTTCAGTGTCTCGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
Db 827 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 846
QY 1564 GAGCAGAACGTCGCCAAGCGCAGTCTCAAGCGGTGGTCAACGCGCCACCATG 1623
Db 847 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 866
QY 1624 TCCACAGTTCACAGNAGGGCACTTCAGGCCCAATGGGAGGCCCAATCAGAGCTG 1683
Db 867 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 886
QY 1684 TGTGAGAACCTGGAGACCCGCTGCTGCTACCAACAGACCTACCTACCTACACCAAC 1743
Db 887 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 906
QY 1744 CATGCCATC 1752
Db 907 HisAlaIle 909
```

```
RESULT 6
AAO15101
ID AAO15101 standard; protein; 909 AA.
XX AAO15101;
AC AAO15101;
DT 29-AUG-2003 (revised)
DT 22-AUG-2002 (first entry)
XX
DE Human phSPmGluR4 chimeric protein.
XX
XX Human; G-protein fusion receptor; extracellular domain;
XX transmembrane domain; intracellular domain; Car; mGluR; GABABR;
XX modulator identification.
XX
XX Homo sapiens.
XX OS Chimeric.
XX WO200229033-A2.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US031074.
XX
XX 03-OCT-2000; 2000US-00679664.
XX
XX (NPSp-) NPS PHARM INC.
XX
XX Stormann T, Hammerland LG, Storjohann LL, Busby JG, Garrett JE;
XX Simin RT;
XX
XX MPI; 2002-330170/36.
XX
XX Novel G-protein fusion receptor, useful for identifying modulators of
XX Car, mGluR and GABABR, comprises G-protein joined to the intracellular
XX domain of the receptor.
XX
XX Disclosure; Fig 16; 168pp; English.
XX
XX The invention comprises G-protein fusion receptors - comprising
XX extracellular, transmembrane and intracellular domains similar to Car,
XX mGluR or GABAB receptor sequences. The G-protein fusion receptors of the
XX invention may also possess a linker joined to the carboxy terminus of the
XX intracellular domain, and a G-protein joined to the linker. The G-protein
XX fusion receptors of the invention are useful for identifying modulators
XX of Car, mGluR and GABABR for use in treating associated conditions. The
XX present amino acid sequence was used in the production of the invention.
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 909 AA;
SQ
Alignment Scores:
Pred. No.: 2.8e-209 Length: 909
Score: 3004.50 Matches: 564
Percent Similarity: 97.77% Conservative: 6
Best Local Similarity: 96.74% Mismatches: 12
Query Match: 90.96% Indels: 1
DB: 5 Gaps: 1
US-10-828-332-6 (1-1755) x AAO15101 (1-909)
QY 7 GGGGTATCATCATCTTTGCCAACGAGGATGACA--TCAGGGTTTCGACCGATCTTCTCC 63
Db 327 GlyAlaValThrIleLeuProLysArgMetSerValargGlyPheAspArgTyrPheSer 346
QY 64 AGCCGACGCTGGACAAACACAGCGCAACATCTGTTTCCGAGTTCTGGAGGACAAAC 123
Db 347 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 366
QY 124 TTCATTGCAAGTTGAGCGCCGCTCAGAGGAGGAGCCATCAGAACTGCAC 183
Db 367 PheHisCysLysLeuSerArgHisAlaLeuLysGlySerHisValLysLysCysThr 386
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QY 184 AACCGAGCGCATCGGCGAGGACTCGGCTATGACGAGGAGGAAAGTGCGTCTG 243
 Db 387 AsnArgGluArgIleGlyGlnAspSerAlaTyfGluGlnGluGlyLysValGlnPheVal 406
 QY 244 ATTGACGCTGTGTACGCGCATGGGCGCACGCGCTCACGCCATGACCGTGCACCTGTCTCC 303
 Db 407 IleAspAlaValTyfAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCyPro 426
 QY 304 GCGCGCTAGGACTCTGCCTCGCATGCGACCCCGTGGATGGCACCAGCTGTCTTAAGTAC 363
 Db 427 GlyArgValGlyLeuCyProArgMetAspProValAspGlyThrGlnLeuLeuTyf 446
 QY 364 ATCAGAAAGTCAACTCTCAGGCATGGGGAAACCTGTAACTTCAATGAGAACGGA 423
 Db 447 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 466
 QY 424 GACGACCGGGCGCTACGACATCTACCACTGCACTGCGCAATGCGTCCGCGAGTAC 483
 Db 467 AspAlaProGlyArgTyfAspIleTyfGlnTyfGlnLeuArgAsnAspSerAlaGluTyf 486
 QY 484 AAGGTCACTCGGCTCGTGGACAGACCACTGCACCTCAGAAATAGAGCGGATGCGTGGCCA 543
 Db 487 LysValIleGlySerTyfAspHisLeuHisLeuArgIleGluArgMethIleTyfPro 506
 QY 544 GGGAGTGGCAGAGCTGGCGCTCCATCTGCACTGCGCTGCGCGAGCGGGAGCGA 603
 Db 507 GlySerGlyGlnGlnLeuProArgSerIleCySerLeuProCyGlnProGlyGluArg 526
 QY 604 AAGAGACTGTGAAGGGCATGGCTGCTGCTGCACTGCGACCTGCGCCCTGACCGGTACAC 663
 Db 527 LysLysThrValLysGlyMetProCySfTyfPheLysCyGluProCySfThrGlyTyfGln 546
 QY 664 TACCAAGTGGACCGCTACACCTGTAGAGACTGCGCCCTACGACATGCGCGCCACAGAGAAC 723
 Db 547 TyrGlnValAspArgTyfThrCysLysThrCysProTyfAspMetArgProThrGluAsn 566
 QY 724 CGCAGAGCTGCAGCGCCATCCCATCTGTCATGTCAGTGGAGTGGGACTCGCGCGGCGG 783
 Db 567 ArgThrGlyCysArgProIleProIleIleLysLeuGluTyfPglySerProTrpAlaVal 586
 QY 784 CTGCGCTCTCTCTGCGCTGTGGGCGATCGCGCGCCACGCTGTCTGCTGTGTCTCAGTTT 843
 Db 587 LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValIleThrPhe 606
 QY 844 GTGCGCTACAAGCATACCCCATCTCGTCAAGGCGCTCGGCGCGGAACTGAGTACGTGCTG 903
 Db 607 ValArgTyfAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyfValLeu 626
 QY 904 CTGCGCGGCACTTTCTGTGTACGCACTACCTCTCTCATGATCGCAGCGCGGACCTG 963
 Db 627 LeuAlaGlyIlePheLeuCyfTyfAlaThrThrPheLeuMetIleAlaGluProAspLeu 646
 QY 964 GGGACTGTTCCTCGCGCATCTCTCTAGGCTCGGATGAGCATGAGCATGAGTACCGCGCC 1023
 Db 647 GlyThrCysSerLeuArgIlePheLeuGlyLeuGlyMetSerIleSerTyfAlaAla 666
 QY 1024 CTGCTGACCAAGAACCGCATTTACCGCATCTTTGACGAGGCGAAACGTCGGTCACT 1083
 Db 667 LeuLeuThrLysThrAsnArgIleTyfArgIlePheGluGlnGlyLysArgSerValSer 686
 QY 1084 GCGCGCGTTTCATCAGCGCGCTCGAGCTGGGCATCACCTTCATCTCTCCCTG 1143
 Db 687 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 706
 QY 1144 CAGTCTCGGCATCTGCGTGTGTCTGCTGGAGCCCTCCCATCTCGTGTGTGACCTTC 1203
 Db 707 GlnLeuLeuGlyIleCysValTyfPheValValAspProSerHisSerValValAspPhe 726
 QY 1204 CAGGACCAACGACACTTCACCCCGCTTTCAGGGGGGTGTCAAGTGGCAGACTCTCG 1263
 Db 727 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 746
 QY 1264 GACCTGTCTCTCATCTGCGCTGCTGGGCTACAGCATGCTGTGATGCTCAGTGTACTGTG 1323

Db 747 AspLeuSerLeuIleCysLeuLeuGlyTyfSerMetLeuLeuMetValThrCysThrVal 766
 QY 1324 TACGCCATCAAGACCGCGGCGTCCGAGACTTCAACGAGGCGCAAGCCCATCGGCTTC 1383
 Db 767 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 786
 QY 1384 ACCATGTACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
 Db 787 ThrMetTyfThrThrCysIleValTyfLeuAlaPheIleProIlePhePheGlyThrSer 806
 QY 1444 CAGTCAGCGCAAGCTGTACATCCAGACCAACCACTGAGCGTCTCCGTGAGTCTGAGC 1503
 Db 807 GlnSerAlaAspLysLeuTyfIleGlnThrThrThrLeuThrValSerValSerLeuSer 826
 QY 1504 GCTTCAGTGTCTCGGCGATGCTTACATGCTCCCAAGTCTACATCATCTCTTCCACCCG 1563
 Db 827 AlaSerValSerLeuGlyMetLeuTyfMetProLysValTyfIleLeuPheIlePro 846
 QY 1564 GAGCAGACGTGCCCAAGCGCAGTCTCAAGCGGTGCTCAAGCGGTGCTCAAGCGGTG 1623
 Db 847 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 866
 QY 1624 TCCAACTAGTTCACACAGAGCGCACTTCAGGCGCAATGGGAGGCCAATCAGAGCTG 1683
 Db 867 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 886
 QY 1684 TGTGAGAACCTGAGACCGCCAGCGTGTGCTTACCAACAGACCTAGCTACCTACACCAAC 1743
 Db 887 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyfValThrThrAsn 906
 QY 1744 CATGCCATC 1752
 Db 907 HisAlaIle 909
 RESULT 7
 AAR82658
 ID AAR82658 standard; protein; 912 AA.
 XX
 AC AAR82658;
 XX
 DT 20-DEC-1995 (first entry)
 XX
 DE Human mGluR4.
 XX
 KW Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;
 KW Alzheimer disease; detection; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Domain
 FT
 FT 588..610 Location/Qualifiers
 FT /label= TMD-I
 FT /note= "transmembrane domain I"
 FT 625..645
 FT /label= TMD-II
 FT /note= "transmembrane domain II"
 FT 657..675
 FT /label= TMD-III
 FT /note= "transmembrane domain III"
 FT 699..720
 FT /label= TMD-IV
 FT /note= "transmembrane domain IV"
 FT 751..771
 FT /label= TMD-V
 FT /note= "transmembrane domain V"
 FT 786..807
 FT /label= TMD-VI
 FT /note= "transmembrane domain VI"
 FT 823..847
 FT /label= TMD-VII
 FT /note= "transmembrane domain VII"
 FT
 FT XX

QY 1624 TCACAACTTCCACAGAGGCGCAACTTTCAGGCCCAATGGGGAAGCCAAATCAGAGCTG 1683
 DB 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
 QY 1684 TGTGAGAACTCGAGACCCAGCGCTGCTACCAACAGACCTACCTACCTACCCAC 1743
 DB 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
 QY 1744 CATGCCATC 1752
 DB 910 HisAlaIle 912

RESULT 8

AAE23757
 ID AAE23757 standard; protein; 912 AA.

XX AAE23757;

XX 10-SEP-2002 (first entry)

XX Human metabotropic glutamate (mGluR4) receptor protein.

XX Human; metabotropic glutamate receptor; mGluR4; neurodegeneration;
 KW antipsychotic; anticonvulsant; analgesic; antidepressant; antiemetic.

XX Homo sapiens.

XX US6384205-B1.

XX 07-MAY-2002.

XX 18-AUG-2000; 2000US-00641318.

XX 12-MAR-1996; 96US-0013189P.

XX 12-MAR-1997; 97US-00816178.

XX (ELIL) LILLY & CO ELI.

XX Belagaje RM, Wu S;

XX WPI; 2002-442818/47.

XX N-PSDB; AAD38024, AAD38025.

XX New nucleic acid encoding human metabotropic glutamate receptor, useful
 PT e.g. in screening for specific agonists and antagonists for treating e.g.
 PT neurodegeneration.

XX Claim 1; Col 9-16; 35pp; English.

XX The present invention relates to human metabotropic glutamate receptor
 CC (mGluR4) proteins and polynucleotides encoding such proteins. mGluR4
 CC sequences of the invention are useful for treating acute and chronic
 CC neurodegeneration. They are also used as antipsychotic, anticonvulsant,
 CC analgesic, antidepressant and antiemetic agents. They are also useful for
 CC the diagnosis and/or treatment of conditions associated with an excess or
 CC deficiency of mGluR4. The present sequence is human mGluR4 protein

XX Sequence 912 AA;

Alignment Scores:

Pred. No.: 2,81e-209 Length: 912
 Score: 3004.50 Matches: 564

Percent Similarity: 97.77% Conservativity: 6

Best Local Similarity: 96.74% Mismatches: 12

Query Match: 90.96% Indels: 1

DB: 5 Gaps: 1

US-10-828-332-6 (1-1755) x AAE23757 (1-912)

QY 7 GGGGTATCATCATCTTTGGCAACGAGGATGACA---TCAGGTTTCAGCCGATCTCTCC 63
 DB 330 GlyAlaValThrIleLeuProLysArgMetSerValArgPheAspArgTyrPheSer 349

QY 64 AGCCCCACGCTGGACAAACAAAGGCGCAACATCTCGTTTGCAGATTCTTGGAGAGCAAC 123
 DB 350 SerArgThrLeuAspAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
 QY 124 TTCCATTCCAAAGTTGAGCGCCGACCGCTCAAGAGGGAAGCCACATCAAGAAGTGCACC 183
 DB 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr 389
 QY 184 AACCCAGAGCGCATCGGCGCAGACTCGGCCCTATAGACAGAGGAGGGAAGTGCAGTTCTG 243
 DB 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal 409
 QY 244 ATTGACGCTGTGTACGCCCATCGCCGCTGCACGCCATGCACCGTACCTGTGTCTCC 303
 DB 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GCGCGGTAGGACTCTGCCCTCGCATGCACCCCGTGGATGGCACCACCTGCTTAAGTAC 363
 DB 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGGAACGCAACTTCTCAGGCATTGCGGGGAACCTGTAACTTCAATGAGAACGA 423
 DB 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GACGACCGGGCGCTACGACATCTACAGTACCAACTCGCGCAATGGCTCGGCCCGAGTAC 483
 DB 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGTCATCGGCTCGTGACAGACACCTGCACCTCAGANTAGCGGATGAGTGGCCA 543
 DB 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
 QY 544 GGGAGTGGCCAGCAGCTCGCGCTCCATCTGCAGTCTGCCCTGCAGCCCGGGGAGCGA 603
 DB 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAGACTGTAAAGGCGATGCTTGTGTGGCACTCGAGCCCTGCACCGGGTACCAG 663
 DB 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATCGGCGCCACAGAAC 723
 DB 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGAGCTGCAGCCCATCCCATCTCAAGTTGGAGTGGGAGCTCGCGTGGCGCGTG 783
 DB 570 ArgThrGlyCysArgProIleProIleLysLeuGluTrpGlySerProTrpAlaVal 589
 QY 784 CTGCCCTCTTCTGCGCGTGGGCACTCGCCGACCTGCTTTCGTGGTGGTCACTGTTT 843
 DB 590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
 QY 844 GTGGCTTACAAGATACCCCATCGTCAAGCGCTCGGCGCGGAACTAGCTACCTGCTG 903
 DB 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
 QY 904 CTGGCGGCGCATCTTCTGTGCTAGCCCACTACTCTTCTCATGTCGACAGCGCGACCTG 963
 DB 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
 QY 964 GGGACCTGTTCTGCTCCGCGCATCTTCTTAGGGCTCGGCATGAGCATCAGCTACCGGCC 1023
 DB 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
 QY 1024 CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTTGGACGAGGGAACCGTCCGTCA 1083
 DB 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
 QY 1084 GCCCGCGCTTTCATCAGCCCGCGCTCGCAGCTGGCCATCACCTTCATCTCTCCCTG 1143
 DB 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709

QY 1684 TGTGAGAACTGAGACCCAGCGCTGGCTACCAAAAGACCTACCTACCTACCAAC 1743
 |||||
 DB 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
 |||||

QY 1744 CATGCCATC 1752
 |||||
 DB 910 HisAlaIle 912
 |||||

RESULT 11

AD58166
 ID AD58166 standard; protein; 912 AA.

XX AC AD58166;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein Q14833, SEQ ID NO 4037.

XX KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GENO) GEN HOSPITAL CORP.

XX PA (PARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX DR GENBANK; Q14833.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 912 AA;

Alignment Scores:
 Pred. No.: 2,81e-209 Length: 912
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 90.96% Indels: 1
 DB: 7 Gaps: 1

US-10-828-332-6 (1-1755) x AD58166 (1-912)

QY 7 GGGGTATCATCTTTTCCCAACGAGGATGACA---TCAGGTTTCGACCGATACTTCTCC 63
 |||||
 DB 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 |||||
 QY 64 AGCCGACGCTGGACAAACAACAGGCGCAATCTCGTTTTCGAGATTCTGGGAGGACAAC 123
 |||||
 DB 350 SerArgThrLeuAspAsnArgArgAenilleTrrPheAlaGluPheTrrPgluAspAen 369
 |||||
 QY 124 TTCATTGCAAGTTGAGCGCGCACGCGCTCAGAGAGGAGCCACATCAAGAGTGCACC 183
 |||||
 DB 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysCysThr 389
 |||||
 QY 184 AACCGAGAGCGCATCGGCGAGGACTCGCGCTATGACGAGGAGGAGGAGGAGTGCAGTTCGTG 243
 |||||
 DB 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyValGlnPheVal 409
 |||||
 QY 244 ATTGACGCTGTGACGCCATCGGCGCACGCGCTGACGCCATGACCGTGACTGTGTCCC 303
 |||||
 DB 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 |||||
 QY 304 GGCGCGTAGGACTCTGCCCTCGCATGACACCCCGTGGATGGCACCCAGCTGCTTAAGTAC 363
 |||||
 DB 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 |||||
 QY 364 ATCAGGAACGTCACCTCTCAGGCAATTCGGGGAGACCTGTAACTTCAATGAGAACGGA 423
 |||||
 DB 450 IleArgAnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAnGly 469
 |||||
 QY 424 GACGACCGGGCGCTACGACATCTACAGTACCAACTGCCCAATGGCTCGGCGCGAGTAC 483
 |||||
 DB 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 |||||
 QY 484 AAGTCTCGGCTGTGGACAGACACCTGCACCTCAGACATAGACCGGATGCGAGTGGCCA 543
 |||||
 DB 490 LysValIleGlySerTrrThrAspHisLeuHisLeuArgIleGluArgMetHisTrrPro 509
 |||||
 QY 544 GGGAGTGCCAGCAGCTCGCGCTCCATCTGCAGTCTGCCCTGCAGCCCGGGGAGGGA 603
 |||||
 DB 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 |||||
 QY 604 AAGAAGACTGTGAAGGGCATGGCTGTGCTGGCATCGAGCCCTGACCGGGTACGAG 663
 |||||
 DB 530 LysLysThrValLysGlyMetProCysCysTrrHisCysGluProCysThrGlyTyrGln 549
 |||||
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACTGCCCTACGACATGCGGCGCCACAGAGAAC 723
 |||||
 DB 550 TyrGlnValAspArgTrrThrCysLysThrCysProTyrAspMetArgProThrGluAn 569
 |||||
 QY 724 CGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAGTGGAGCTCCCGTGGCGCGGTG 783
 |||||
 DB 570 ArgThrGlyCysArgProIleProIleLysLeuGluTrrPglYserProTrrPalaVal 589
 |||||
 QY 784 CTGCGCCCTCTTCTCGCGCGTGGTGGGATCCCGCACGCTGTTCTGGTGGTCACTGTTT 843
 |||||
 DB 590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
 |||||
 QY 844 GTGGCTTACAACGATACCCCATCGTCAAGCGCTCGGCGCGGAGAACTAGCTAGCTGCTG 903
 |||||

Db 610 ValArgTyrAsnAspThrProileValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
Qy 904 CTGGCGGCGATCTTTCTGCTACCGCCACTCTCTCATGATCGCAGACGCGACCTG 963
Db 630 LeuAlaGlyIlePheLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 649
Qy 964 GGGACCTGTTGCTCGCGCGATCTCTCTAGCGCTCGGCATGAGCATCAGCTACGCGGCC 1023
Db 650 GlyThrCysSerLeuArgGlyIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
Qy 1024 CTGCTGACACAGCAACCGCATTTACCGCATCTTTGAGCAGGGCAACCGTGGTCACT 1083
Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
Qy 1084 GCCCGCGCTTTCATCAGCCGCGCTCGCAGCTGGCCATCAGCTTCATCTCATCTCCCTG 1143
Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
Qy 1144 CAGCTGCTCGGATCTGCGTGTGGTTCGTGTGGAGCCCTCCACTCGGTGGTGGACTTC 1203
Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
Qy 1204 CAGGACCAACGACACTTGTACCCCGCTTTGCGAGGGCGTCTCAAGTGGCAGCATCTCG 1263
Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
Qy 1264 GACCTGCTCCCTCATCTGCTGCTGGCTACAGCATGCTGCTGCTGCTGCTGCTGCTGCTG 1323
Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuMetValThrCysThrVal 769
Qy 1324 TACGCCCATCAGACCCGAGCGCTGCGCGAGACCTTCAACGAGGCCCAACCCATCGGCTTC 1383
Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
Qy 1384 ACCATGTACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
Qy 1444 CAGTCAGCGCAGCAAGCTGTACATCCAGACACACACACACACACACACACACACACAC 1503
Db 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 829
Qy 1504 GCTTCAGTGTCTCTCGGATGCTGTACATGCGCCAAAGCTCATCATCTCTTCTCCACCG 1563
Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLysPheIlePro 849
Qy 1564 GAGCAGACGTGCCCAAGCGCAGCTCTCAAGCGGTGTCACCGCGCCACCATG 1623
Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
Qy 1624 TCCACAAAGTTCACAGAGGGCAACTTCAGGCCCATGGGAGCCCAATCAGAGCTG 1683
Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
Qy 1684 TGTGAGAACCTGGAGACCCCGCTGGCTGTACCAACAGACCTAGCTCACCTACACCAAC 1743
Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
Qy 1744 CATGCCATC 1752
Db 910 HisAlaIle 912
RESULT 12
ADO29094
ID ADO29094 standard; protein; 912 AA.
XX
AC ADO29094;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human novel GPCR GRM4, SEQ ID NO:193.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;

transgenic mouse; neurological disorder; adrenal gland disorder;
colon disorder; intestinal disorder; cardiovascular disorder;
muscular disorder; blood disorder; immune disorder; bone disorder;
joint disorder; metabolic disorder; nutritive disorder; cancer;
kidney disorder; liver disorder; lung disorder; breast disorder;
ovary disorder; uterus disorder; prostate disorder; testis disorder;
skin disorder; stomach disorder; pancreas disorder; spleen disorder;
thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
cytostatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;
CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
dermatological; antiulcer; antithyroid; antiallergic; anorectic;
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
receptor.
Homo sapiens.
WO2004040000-A2.
13-MAY-2004.
09-SEP-2003; 2003WO-US028226.
09-SEP-2002; 2002US-0409303P.
09-APR-2003; 2003US-0461329P.
(PRIM-) PRIMAL INC.
Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
WPI; 2004-390329/36.
N-PSDB; ADO29776.
Novel mammalian G protein coupled receptors, useful for identifying
compounds that modulates diagnosing and treating disease condition
associated with GPCR dysfunction e.g. autoimmune diseases, angina
pectoris, Parkinson's disease.
Claim 1; SEQ ID NO 193; 542pp; English.
The invention relates to human and mouse G protein-coupled receptors
(GPCRs) and nucleic acids encoding them. The invention also relates to
sequences at least 90% identical to the GPCR proteins and nucleic acids
of the invention; methods of treating, preventing or diagnosing diseases
associated with GPCRs of the invention; methods of screening for
compounds useful in the treatment of GPCR-related diseases; a transgenic
mouse comprising a GPCR gene of the invention; a mouse comprising a
mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
from the transgenic mice; kits comprising several mice, each of which has
a mutation in a different GPCR gene of the invention; and kits comprising
probes which hybridise to GPCR polynucleotides of the invention. The
invention further discloses variants of the GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
diseases including neurological disorders (e.g., Alzheimer's disease,
depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
disorders of the adrenal gland; disorders of the colon or intestine
(e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
myocardial infarction); muscular disorders; blood disorders (e.g.,
anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
obesity, enzyme deficiency-related diseases or vitamin deficiency-related
diseases); and disorders of the kidney, liver, lung, breast, ovary,
uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
thyroid (e.g., cancers). The present sequence represents a GPCR of the
invention. Note: The full sequence data for this patent did not form part
of the printed specification; those sequences not shown were obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 912 AA;
 Alignment Scores:
 Pred. No.: 2,81e-209 Length: 912
 Score: 3004.50 Matches: 564
 Percent Similarity: 97.77% Conservative: 6
 Best Local Similarity: 96.74% Mismatches: 12
 Query Match: 90.96% Indels: 1
 DB: 8 Gaps: 1
 US-10-828-332-6 (1-1755) x ADO29094 (1-912)
 QY 7 GGGGTATCATCTCTTTGCCACGAGATGACA---TCAGGGTTCGACGATCTCTCC 63
 Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCGACCGCTGGACAAACAGCGCAACATCTGGTTTGGCGAGTCTTGGGAGGACAAC 123
 Db 350 SerArgThrLeuAspAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
 QY 124 TTCCATTGCAAGTTGAGCCGCCACCGCTCAAGAGGGAAGCCACATCAAGAGTGCAAC 183
 Db 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr 389
 QY 184 AACCGAGCGCATCGGCGAGAGCTCGGCTATGACGAGGAGGAGGTGCAAGTTCGTG 243
 Db 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
 QY 244 ATTGAGCGTGTGACGCCATGGCCACGCGCTGCAGCGCATCACCGTCACTGTGTC 303
 Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GGCGCGTGAAGTCTGCGCTCGCATGGACCCCGTGGATGGCACCCAGCTGCTTAAGTAC 363
 Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGGAAGCTCAACTTCAGCATTTGGGGGAACCTGTAACTTCAATGAGAACGGA 423
 Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GACGACCGGGCGCTTACCATCTACAGTACCACTACCACTGCGCAATGGCTCGGCCGAGTAC 483
 Db 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGGTGATCGGTCTGTGGACAGACACCTGCACCTCAGAAATAGAGCGCATGCGAGTGGCCA 543
 Db 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMethIstTrpPro 509
 QY 544 GGGAGTGGCAGAGCTCGCGCTCCATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
 Db 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAGACTGTGAAGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
 Db 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGCGCTTACACTGTGAAGCTGCGCTTACGACATGCGGCCACACAGAGAAC 723
 Db 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CCGCAGAGTGGCAGCCCATCCCATCTGTCAGTGTGAGTGGAGTGGAGTGGAGTGGAGTGG 783
 Db 570 ArgThrGlyCysArgProIleIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
 QY 784 CTGCCCCCTCTCTGCGCGTGTGGCATCGCGCGCATCGCGCTGCTGCTGCTGCTGCTGCTG 843
 Db 590 LeuProLeuPheLeuAlaValGlyIleAlaAlaThrLeuPheValIleThrPhe 609
 QY 844 GTGCGCTACCAAGATACCCCATCTGTCAGAGGCTCGGGCCGGCAACTGAGCTACGTGCTG 903
 Db 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
 QY 904 CTGGCGGGCATCTTTCTGTGTACGCCACTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 963

Db 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
 QY 964 GGGAGCTGTTCCTCGCGCGCATCTTCTTAGGCGCTCGGCATGAGCATGAGTACGCGGCC 1023
 Db 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
 QY 1024 CTGCTGACCAAGACCAACCGCATTTACCGCATCTTTTGAGCAGGCAACCGTGGTCACT 1083
 Db 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
 QY 1084 GCCCGCGCTTTCATCAGCCCGCGCTCGCAGCTGGCCATCACCTCTCATCTCTCCCTG 1143
 Db 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
 QY 1144 CAGCTGCTCGGCATCTGCGTGTGGTTCGTGGTGGACCCCTCCCATCTCGGTGGTGA 1203
 Db 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
 QY 1204 CAGGACCAACCGACACTTTCACCCCGCTTTGCCAGGGCGTCTCAAGTGCACATCTCG 1263
 Db 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
 QY 1264 GACCTGCTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
 Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
 QY 1324 TACGCCATCAAGACCCGAGGGGTGCCGAGACCTTCAACGAGGCGCAAGCCCATCGGCT 1383
 Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
 QY 1384 ACCATGTACACCACTGCACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
 Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 809
 QY 1444 CAGTCAGCGGACAGCTGTACATCCAGACCAACCACTGAGCGGTCTCGTGGTCTGAGC 1503
 Db 810 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GCTTCAGTGTCTCGGGATGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563
 Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHisPro 849
 QY 1564 GAGCAGAACGTGCCCAAGCGCAGTCTCAAGCGGTGGTCCACCGCCGCCACCATG 1623
 Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 869
 QY 1624 TCCAAACAGTTCAACAGAGGGCACTTTCAGGCCCAATGGGGAAGCCCAATCAGAGCTG 1683
 Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
 QY 1684 TGTGAGAACCTGGAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1743
 Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
 QY 1744 CATGCCATC 1752
 Db 910 HisAlaIle 912
 RESULT 13
 ADO89114
 ID ADO89114 standard; protein; 912 AA.
 XX
 AC ADO89114;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human urological disorder related protein 115 SEQ.66.
 XX
 KW urological disorder; uropathic; cytostatic; urinary incontinence;
 KW benign prostatic hyperplasia; human.
 XX
 OS Homo sapiens.

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XX WO2004065576-A2.
PN
XX
XX PD
XX PF
XX PP
XX PR
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-0488529P.
PR 30-JUL-2003; 2003US-0491156P.
PR 02-SEP-2003; 2003US-0499594P.
PR 26-SEP-2003; 2003US-0506332P.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Karicheti V, Silos-Santiago I, Eliasof SD;
XX
XX WPI; 2004-562167/54.
XX N-PSDB; ADQ89113.
XX
XX Use of polypeptides related to urological disorders, e.g. 44390, 54181,
XX 211 or for identifying a compound capable of treating a urological
XX disorder or identifying and treating a subject having a urological
XX disorder.
XX
XX Claim 1; SEQ ID NO 66; 542pp; English.
XX
XX The present invention describes the use of polypeptides related to
XX urological disorders for identifying a compound capable of treating a
XX urological disorder, identifying a subject having a urological disorder,
XX or treating a subject having a urological disorder. Also described: (1) a
XX method for identifying a compound capable of treating a urological
XX disorder; (2) a method for identifying a subject having a urological
XX disorder; and (3) a method for treating a subject having a urological
XX disorder. The compound has uropathic and cytosolic activities. The
XX polypeptides related to urological disorders are useful for identifying a
XX compound capable of treating a urological disorder, identifying a subject
XX having a urological disorder, or treating a subject having a urological
XX disorder. Disorders include urinary incontinence and benign prostatic
XX hyperplasia. The present sequence represents a human urological disorder
XX related protein, which is used in the exemplification of the present
XX invention.
XX
XX SQ Sequence 912 AA;
XX
XX Alignment Scores:
XX Pred. No.: 2,81e-209 Length: 912
XX Score: 3004.50 Matches: 564
XX Percent Similarity: 97.77% Conservative: 6
XX Best Local Similarity: 96.74% Mismatches: 12
XX Query Match: 90.96% Indels: 1
XX DB: 8 Gaps: 1
XX
XX US-10-828-332-6 (1-1755) x ADQ89114 (1-912)
XX
XX 7 GGGGTATCATCATCTTTCCCAACGAGGATGACA---TCAGGGTTCCGACCATCTTCTCC 63
XX
XX 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAsnArgTyrPheSer 349
XX
XX 64 AGCCGACGCTGGACAACACGAGCGCAACATCTGGTTTGGCGAGTTCTGGGAGGACAAC 123
XX
XX 350 SerArgThrLeuAspAsnArgAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
XX
XX 124 TTCATTTCAGTTGAGCGCGCACCGCTCAAGAGGGAAGCCATCAAGAGTGCACC 183
XX
XX 370 PheHisCysLysLeuSerArgHisAlaLeuLysLysGlySerHisValLysLysCysThr 389
XX
XX 184 AACCGAGAGCGCATCGGGCAGGACTCGGCCTATGAGCAGGAGGGGAGGTCAGTTCTGTG 243
XX
XX AsnArgGluArgIleGlyGlnAspSerAlaTyrGlnGlnGluGlyLysValGlnPheVal 409
XX
XX 244 ATTGACCGCTGTATAGCCATGGCCACCGCTGCACGCCATGCACCGTACCTGTGCCCC 303
XX
XX 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
XX
XX 304 GCGCGCTAGGACTCTCCCTCGCATGGACCCCGTGGATGGCACCAGCTCTTAAAGTAC 363
XX
XX 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
XX
XX 364 ATCAGGAACGTCAACTTCTCAGCATTCGCGGGAACCTGTAACTTCAATGAGAACGGA 423
XX
XX 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
XX
XX 424 GACGACCGGGCGCTAGCAGCATCTACAGTACCACCTGCGCATGGCTGGCCGAGTAC 483
XX
XX 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
XX
XX 484 AAGGTATCGCTCGTGGACAGACCTGTCACCTCAGAAATAGAGCGGATGCAGTGGCCA 543
XX
XX 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
XX
XX 544 GGGAGTGGCCAGCAGCTGCCCGCTCCATCTGCAGTCTGCCCTCCAGCCCGGGAGGGA 603
XX
XX 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
XX
XX 604 AAGNAGACTGTAAGGCGATGGCTGTGCTGGCAGCTGCGAGCCCTGCACGGGTACGAG 663
XX
XX 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
XX
XX 664 TACCAGTGGACGCTACACTGTAAAGACCTGCCCTACGACATGCGGCCCCACAGAGAAC 723
XX
XX 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
XX
XX 724 CGCAGCAGCTGCCACCCATCCCATCGTCAAGTTGGAGTGGGACTCGCCGTGGCCGTG 783
XX
XX 570 ArgThrGlyCysArgProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
XX
XX 784 CTGCCCCCTCTTCTGGCGGTGGTGGGATCGCCCGCAGCTGTTCGTGGTGCACGTTT 843
XX
XX 590 LeuProLeuPheLeuAlaValAlaGlyIleAlaAlaThrLeuPheValIleThrPhe 609
XX
XX 844 GTGGCTACAAACGATACCCCATCGTCAAGCCCTCGCGCGGGAACCTGAGTACGTGCTG 903
XX
XX 610 ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
XX
XX 904 CTGCGCGGCTCTTTCTGTGCTACGCCACTACCTTCTCTCATGATCGCAGAGCCGAGCTG 963
XX
XX 630 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 649
XX
XX 964 GGGACCTGTTCGCTCCCGCGCATCTTCTAGGGCTCGGCATGAGCATCAGCTAGCGGCC 1023
XX
XX 650 GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
XX
XX 1024 CTGCTGACCAAGCAACACCGCATTTTACCGCATCTTTTCCAGAGGGGCAACCGTCCGTCAGT 1083
XX
XX 670 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
XX
XX 1084 GCGCGCGCTTTCATPACGCCCGCGCTCGCAGCTGCCATCATCTTCTCATCTCTCCCTG 1143
XX
XX 690 AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
XX
XX 1144 CAGTGTCTGGCATCTCGGTGTGGTTCGTGGTGGACCCCTCCCATCGGTGGTGGACTTC 1203
XX
XX 710 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
XX
XX 1204 CAGGACCAACGAGCACCTTGAACCCCGCTTTGCCAGGGCGCTCAAGTGCAGCATCTCG 1263
XX
XX 730 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 749
XX
XX 1264 GACCTGTCCCTCATCTCTGCTGCTGGGTACAGCATGCTGTGATGGTGCAGCTGCTGTG 1323
XX
XX
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Db 750 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
 QY 1324 TAGCCATCAAGACCGAGCGTCCGAGAGCTTCAACGAGCGCAAGCCCATCGCTTC 1383
 Db 770 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
 QY 1384 ACATGTATACACCTGCTATGTTGCTGGCTGGCTTCATCCCATCTTTTGGCAGCTCA 1443
 Db 790 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
 QY 1444 CAGTCAGCGACAAAGCTGTACATCCAGACACACACTGACCGTCTCCGTGAGTCTGAGC 1503
 Db 810 GlnSerAlaAspLysLeuIleGlnThrThrLeuThrValSerValSerLeuSer 829
 QY 1504 GCTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAGTCTACATCATCTCTTCCACCGG 1563
 Db 830 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
 QY 1564 GAGCAGAACGTCGCCAAGCGCAGCGCAGTCTCAAGCGGTGTGTCACCGCGCCACCATG 1623
 Db 850 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
 QY 1624 TCCAAACAGTTTCCACAGAGGCGCACTTCAGSCCAATGGGGAAGCCCAATCAGAGCTG 1683
 Db 870 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
 QY 1684 TGTGAGAACCTGGAGACCCGAGCGCTGTACCAACAGACCTTACGTCACCTACACCAAC 1743
 Db 890 CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrThrAsn 909
 QY 1744 CATGCCATC 1752
 Db 910 HisAlaIle 912

RESULT 14
 ID AAR72092 standard; protein; 912 AA.
 AC AAR72092;
 XX 25-MAR-2003 (revised)
 DT 26-SEP-1995 (first entry)
 XX Human mGluR4.
 XX Human metabotropic glutamate receptor subtype 4; mGluR4; hmGluR4;
 KW signal transducer.
 XX Homo sapiens.
 XX WO9508627-A1.
 XX 30-MAR-1995.
 PF 07-SEP-1994; 94WO-BP002991.
 XX 20-SEP-1993; 93BP-00810663.
 PR 19-AUG-1994; 94GB-00016553.
 XX (CIBA) CIBA GEIGY AG.
 XX Flor PJ, Kuhn R, Lindauer K, Puettner I, Knoepfel T;
 DR WPI: 1995-139596/18.
 DR N-PSDB; AAQ89342.
 XX Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and 7 - also
 PT corresp. DNA and antibodies, useful for identifying cpds. which modulate
 PT signal transduction activity.
 XX Claim 2; Page 44-48; 110pp; English.
 XX Human metabotropic glutamate receptor subtype 4 (hmGluR4) cDNA clones

CC were isolated from a cerebellum cDNA library using a rat mGluR4 probe.
 CC Clone cMR20 lacked the 5' end of the hmGluR4 gene. PCR using human
 CC genomic or brain cDNA as template was used to obtain a complete gene
 CC sequence [given in AAQ89342] encoding hmGluR4 (AAR72092). Recombinant
 CC hmGluR4 was produced in mammalian cells. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX SQ Sequence 912 AA;

Alignment Scores:

Pred. No.: 4,648-209 Length: 912
 Score: 2001.50 Matches: 563
 Percent Similarity: 97.77% Conservative: 7
 Best Local Similarity: 96.57% Mismatches: 12
 Query Match: 90.87% Indels: 1
 DB: 2 Gaps: 1

US-10-828-332-6 (1-1755) x AAR72092 (1-912)

QY 7 GGGGTATCATCATCTTTGCCAACGAGGATGACA---TCAGGGTTGACCGATCTCTCTCC 63
 Db 330 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 349
 QY 64 AGCCGACGCTGCACAAACAGGCGCACATCTGTTTCCGAGTCTCTGGGAGGACAC 123
 Db 350 SerArgThrLeuAspAsnAsnArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 369
 QY 124 TTCCATTGCAAGTTGAGCGCCACCGCTCAAGAGGGAAGCCACATCAAGAGTGCACC 183
 Db 370 PheHisCysLeuLeuSerArgHisAlaLeuLysGlySerHisValLysCysThr 389
 QY 184 AACCCAGAGCGCATCGGCGAGACTCGGCCTATAGACAGGAGGGAAGGTGCAGTTCTGTG 243
 Db 390 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 409
 QY 244 ATTGACGCTGTGTACGCCATGCGCCACCGCTGCAGCGCATCACCGTGCACCTGTCTCC 303
 Db 410 IleAspAlaValTyrAlaMetGlyHisAlaLeuHisAlaMetHisArgAspLeuCysPro 429
 QY 304 GCGCGCTAGGACTCTGCGCTCGCATGACCCCGTGGATGGCACCAGCTGCTTAAGTAC 363
 Db 430 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 449
 QY 364 ATCAGAAACGTCAACTTCTCAGGCAATTCGGGGAAACCTGTAACTTCAATGAGAACGGA 423
 Db 450 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 469
 QY 424 GAGCACCAGCGCGCTACGACATCTACAGTACCAACTGCGCAATGGCTCGGCCGAGTAC 483
 Db 470 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 489
 QY 484 AAGGTCATCGCTCGTGACAGACACCTGCACCTCAGAATAGAGCGGATGCAGTGGCCA 543
 Db 490 LysValIleGlySerTrpThrAspHisLeuHisLeuArgIleGluArgMetHisTrpPro 509
 QY 544 GGGAGTGGCCAGCAGCTCGCGCTCCCATCTGCACTCTGCTCCCTGCGCAGCCGCGGAGCGA 603
 Db 510 GlySerGlyGlnGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 529
 QY 604 AAGAAGACTGTGAAGGGCATGCTTGTCTGGCACTGGGAGCCCTGCACCGGGTACCAG 563
 Db 530 LysLysThrValLysGlyMetProCysCysTrpHisCysGluProCysThrGlyTyrGln 549
 QY 664 TACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTACGACATCGCGCCACACAGAAC 723
 Db 550 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 569
 QY 724 CGCAGAGCTGCACGCCCATCCCATCGTCAAGTTGGAGTGGGACTCGCGTGGGCGGTG 783
 Db 570 ArgThrGlyCysArgProIleProIleIleLysLeuGluTrpGlySerProTrpAlaVal 589
 QY 784 CTGCCCTCTTCTCGCTGGCGTGGGATCGCCGACGCTTCTCGTGGTGTCTACGTTT 843

Db LeuProLeuPheLeuAlaValValGlyIleAlaAlaThrLeuPheValValIleThrPhe 609
QY 844 GTGGCTACACGATACCCCATCGTCAAGCCTCGGCGGCACTGAGTACGTGCTG 903
Db ValArgTyrAsnAspThrProIleValLysAlaSerGlyArgGluLeuSerTyrValLeu 629
QY 904 CTGGGGGCATCTTTCTGTGTGTACGCCACTACCTTCTCATGATCGCAGACCGGACCTG 963
Db LeuAlaGlyIlePheLeuLeuCysTyrAlaThrPheLeuMetIleAlaGluProAspLeu 649
QY 964 GGGACCTGTTCTGCTCCGCGCATCTTCTCAGGCTCGGCATCAGCATCAGCTACGCGCC 1023
Db GlyThrCysSerLeuArgArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 669
QY 1024 CTGCTGACCAACCAACCGCATTTACCGCATCTTTGAGCAGGCGCAACGCTCGTCAGT 1083
Db LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 689
QY 1084 GCCCGCGTTCATCAGCCGCGCTCGCAGCTGGCATCACCTTCATCTCATCTCCCTG 1143
Db AlaProArgPheIleSerProAlaSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 709
QY 1144 CAGCTGCTCGGCATCTGCTGTGTGTGTGTGGACCCCTCCACTCGGTGTGTGACTTC 1203
Db GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHisSerValValAspPhe 729
QY 1204 CAGGACCAACGACACTTACCCCGCTTTCGAGGGCGGTGCTCAAGTGGACATCTCG 1263
Db GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspMetSer 749
QY 1264 GACCTGCTCCCTCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1323
Db AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 769
QY 1324 TACGCCATCAAGACCCGAGGGGTGCGCCGAGACCTTCAACGAGGCGCAACCCATCGCTTC 1383
Db TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 789
QY 1384 ACCATGTACACCATCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1443
Db ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePheGlyThrSer 809
QY 1444 CAGTCAGCGGCAACGCTGTACATCCAGACCAACCACTGAGCTCTCGTGTGTGTGTGAGC 1503
Db GlnSerAlaAspLysLeuTyrIleGlnThrThrThrLeuThrValSerValSerLeuSer 829
QY 1504 GCTTCAGTGTCTCTGGGATGCTGTACATGCCCAAGTCTACATCATCTCTTCCACCCG 1563
Db AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleIleLeuPheHisPro 849
QY 1564 GAGCAGACGTGCCCAAGCGGACGCGAGTCTCAAGCGGTGTGTGTGTGTGTGTGTGTGT 1623
Db GluGlnAsnValProLysArgLysArgSerLeuLysAlaValValThrAlaAlaThrMet 869
QY 1624 TCACCAAGTTCCACAGAGGCACTTTCAGGCCCAATGGGAGGCGCAAAATCAGAGCTG 1683
Db SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 889
QY 1684 TGTGAGAACCTGTGAGACCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1743
Db CysGluAsnLeuGluAlaProAlaLeuAlaThrLysGlnThrTyrValThrTyrThrAsn 909
QY 1744 CATGCCATC 1752
Db HisAlaIle 912

RESULT 15

ID ADR08623 standard; protein; 591 AA.

XX

AC ADR08623;

XX

DT 04-NOV-2004 (first entry)

XX Human protein useful for treating neurological disease Seq 2129.
DE human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nontropic; antiparkinsonian; cytostatic;
KW tranquiliser.
XX Homo sapiens.
OS
XX EPI447413-A2.
FN
XX 18-AUG-2004.
PD
XX 12-FEB-2004; 2004EP-00003145.
PF
XX 14-FEB-2003; 2003JP-00102207.
PR
XX 09-MAY-2003; 2003JP-00131452.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX
XX WPI; 2004-583265/57.
DR N-PSDB; ADR06667.
DR
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX Claim 1; SEQ ID NO 2129; 2686pp; English.
XX This invention relates to novel, isolated full length human cDNA
XX molecules and the encoded proteins thereof. Specifically, it refers to
XX cDNA clones obtained by an oligo-capping method, where none of these
XX clones are identical to any known human mRNAs. The present invention
XX describes an immunoassay to identify agonists and antagonists, as well as
XX antibodies, antisense molecules and siRNAs that can all be used to bind
XX to and modulate expression of the cDNA molecules. As such, these
XX molecules are useful for diagnostic markers or therapeutic targets for
XX the various diseases or morbid states. In particular, they are useful in
XX gene therapy for treating osteoporosis, neurological disease, Alzheimer's
XX disease, Parkinson's disease, dementia, short memory and various cancers,
XX as well as for maintaining equilibrium of sense or motor function, and
XX for treating emotional reaction, fear response and panic. Accordingly,
XX they exhibit osteopathic, neuroprotective, nontropic, antiparkinsonian,
XX cytosstatic and tranquiliser activities. This polypeptide is a protein
XX encoded by a full length human cDNA sequence of the invention. NOTE: This
XX sequence is not given in the sequence listing of the specification but
XX can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
XX office.
SQ Sequence 591 AA;

Alignment Scores:
Pred. No.: 1.19e-202 Length: 591
Score: 2912.50 Matches: 545
Percent Similarity: 97.53% Conservative: 8
Best Local Similarity: 96.12% Mismatches: 13
Query Match: 88.18% Indels: 1
DB: Gaps: 1

US-10-828-332-6 (1-1755) x ADR08623 (1-591)

QY 7 GGGGTATCATCTTTGCCCAACGAGGATGACA---TCAGGGTTCCGACCGATCTCTCC 63

Db 22 GlyAlaValThrIleLeuProLysArgMetSerValArgGlyPheAspArgTyrPheSer 41

QY 64 AGCCGACGCTGGACACACAGCGGCAACATCTGGTTTCCGAGTTCTGGAGGACAC 123

Db 42 SerArgThrLeuAspAsnAsnArgArgAsnIleTrpPheAlaGluPheTrpGluAspAsn 61


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QY 124 TTCCATTGCAAGTTGAGCGCCGCGCTCAGAGAGGGAAGCCACATCAAGAAGTGCACC 183
Db 62 PheHieCysLysLeuSerArgHieAlaLeuLysLysGlySerHieValLysLysCysThr 81
QY 184 AACCCGAGAGCGCATCCGGCAGGACTCGGCTATGAGCAGGAGGGAAGGTGCAGTTCCG 243
Db 82 AsnArgGluArgIleGlyGlnAspSerAlaTyrGluGlnGluGlyLysValGlnPheVal 101
QY 244 ATTGACGCTGTGTACGCCATGGCCACCGGCTGCAGCCATGCACCGTGCACCTGTGTC 303
Db 102 IleAspAlaValTyrAlaMetGlyHieAlaLeuHieAlaMetHieArgAspLeuCysPro 121
QY 304 GGGCGGCTAGGACTCTCCCTCGCATGGACCCCGTGGATGGACCCAGCTGCTTAAGTAC 363
Db 122 GlyArgValGlyLeuCysProArgMetAspProValAspGlyThrGlnLeuLeuLysTyr 141
QY 364 ATCAGGAAGCTCAACTTCTCAGCATTGGGGGGAACCTGTAACTTCAATGAGACCGA 423
Db 142 IleArgAsnValAsnPheSerGlyIleAlaGlyAsnProValThrPheAsnGluAsnGly 161
QY 424 GAGCACCGGGCGCTACACACATCTACACAGTACCAACTGCGCAATGGCTCGGCGCAGTAC 483
Db 162 AspAlaProGlyArgTyrAspIleTyrGlnTyrGlnLeuArgAsnAspSerAlaGluTyr 181
QY 484 AAGGTCAATCGGCTCGTGGAGACACCACTGCACCTCAGAAATAGAGCGGATGCAGTGCCA 543
Db 182 LysValIleGlySerTrpThrAspHieLeuHieLeuArgIleGluArgMethIstTrpPro 201
QY 544 GGGAGTGGCCAGCAGCTCGCGCTCCATCTCGACTGCGCTGCTCCCTGCCAGCCCGGGAGCGA 603
Db 202 GlySerGlyGlnLeuProArgSerIleCysSerLeuProCysGlnProGlyGluArg 221
QY 604 AAGAAGACTGTGAAGGGCATGGCTGCTGCTGCTGCGACTGCGAGCTGCACCGGTACACAG 663
Db 222 LysLysThrValLysGlyMetProCysCysTyrHisCysGluProCysThrGlyTyrGln 241
QY 664 TACCAAGTGGACGCTACACTGTGAAGACTTCGCCCTACGACATCGCGCCCAACAGAGAAC 723
Db 242 TyrGlnValAspArgTyrThrCysLysThrCysProTyrAspMetArgProThrGluAsn 261
QY 724 CCGCAGAGCTGCCAGGCCATCCCATCTCAAGTGGAGTGGAGTCCGCGTGGGCGGTG 783
Db 262 ArgThrGlyCysArgProIleLysLeuGluTrpGlySerProTrpAlaVal 281
QY 784 CTGCCCCCTCTCTCGCGCTGGTGGGCATCGCGCCAGCTGTGTGTGTGTGTACGTTT 843
Db 282 LeuProLeuPheLeuAlaValValGlyIleAlaIaIaThrLeuPheValIleThrPhe 301
QY 844 GTGCGCTACACGATACCCCATCGTCAAGGCTCGGGCCGGAACTGAGCTACGTGCTG 903
Db 302 ValArgTyrAsnAspThrProIleValArgAlaSerGlyArgGluLeuSerTyrValLeu 321
QY 904 CTGGGGGGCATCTTCTGTGTGTACGCCACTACCTTCCTCATATGCAGAGCGGACCTG 963
Db 322 LeuAlaGlyIlePheLeuCysTyrAlaThrThrPheLeuMetIleAlaGluProAspLeu 341
QY 964 GGGACTGTTCCTCGCGCGCATCTTCCTAGGCTCGGCATCAGCATCAGCTACCGGCC 1023
Db 342 GlyThrCysSerLeuArgIlePheLeuGlyLeuGlyMetSerIleSerTyrAlaAla 361
QY 1024 CTGCTGACCAAGACCAACCGCATTTTACCGCATCTTTGAGCAGGCAACCGTCCGTCAGT 1083
Db 362 LeuLeuThrLysThrAsnArgIleTyrArgIlePheGluGlnGlyLysArgSerValSer 381
QY 1084 GCCCGCGTTTCATACGCCCGGCTCGAGCTGGCCATCACCTTCATCTCATCTCCCTG 1143
Db 382 AlaProArgPheIleSerProValSerGlnLeuAlaIleThrPheSerLeuIleSerLeu 401
QY 1144 CAGCTGCTCGGATCTCGTGTGGTTCGTGGTGGACCCCTCCACTCGGTGTGGACTTC 1203
Db 402 GlnLeuLeuGlyIleCysValTrpPheValValAspProSerHieSerValLeuAspPhe 421
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QY 1204 CAGGACCAACGAGACACTTGACCCCCCGCTTTGCGAGGGGGTCTCAAGTGCACATCTCG 1263
Db 422 GlnAspGlnArgThrLeuAspProArgPheAlaArgGlyValLeuLysCysAspIleSer 441
QY 1264 GACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
Db 442 AspLeuSerLeuIleCysLeuLeuGlyTyrSerMetLeuLeuMetValThrCysThrVal 461
QY 1324 TACGCCATCAAGACCCGAGGGCTGCCGAGACCTTTCAACGAGGCCAAGCCCATCGGCTTC 1383
Db 462 TyrAlaIleLysThrArgGlyValProGluThrPheAsnGluAlaLysProIleGlyPhe 481
QY 1384 ACCATGTACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
Db 482 ThrMetTyrThrThrCysIleValTrpLeuAlaPheIleProIlePhePheGlyThrSer 501
QY 1444 CAGTCAGCGGCAAGCTGTACATCCAGAACACACACTGACGGTCTCCGTGAGTCTGAGC 1503
Db 502 GlnSerAlaAspLysLeuTyrIleGlnThrThrLeuThrValSerValSerLeuSer 521
QY 1504 GCTTCAGTGTCCCTGGGGATGCTTACATGCCCCAAAGTCTACATCATCTCTTCCACCCG 1563
Db 522 AlaSerValSerLeuGlyMetLeuTyrMetProLysValTyrIleLeuPheHiePro 541
QY 1564 GAGCAGAACGTGCCCAAGCGCAGTCTCAAAGCGGTGCTGCTGCTGCTGCTGCTGCTG 1623
Db 542 GluGlnAsnValProLysArgLysArgSerLeuLysAlaValThrAlaAlaThrMet 561
QY 1624 TCCCAACAAAGTTCACACAGAGGGCAACTTCAGGCCCAATGGGGAAGCCAAATCAGAG 1683
Db 562 SerAsnLysPheThrGlnLysGlyAsnPheArgProAsnGlyGluAlaLysSerGluLeu 581
QY 1684 TGTGAGAACTGGAGACCCCA 1704
Db 582 CysGluAsnLeuGluAlaPro 588
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Search completed: June 17, 2005, 18:40:29
Job time : 307 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 04:06:08 ; Search time 5983 Seconds
(without alignments)
11165.434 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 1755

Sequence: 1 atgcaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	841.4	47.9	3675	3 AK038395	AK038395 Mus muscu
2	841.4	47.9	3693	3 BC051384	BC051384 Mus muscu
3	823.2	46.9	2748	9 AY401210	AY401210 Mus muscu
4	822.6	46.9	3399	3 BC034118	BC034118 Mus muscu
5	807.2	46.0	2748	9 AY401208	AY401208 Homo sapi
6	806.2	45.9	2667	9 AY406145	AY406145 Mus muscu
7	801	45.6	2671	9 AY406143	AY406143 Homo sapi
8	793.8	45.2	4209	3 AK053447	AK053447 Mus muscu
9	788.2	44.9	2611	9 AY401209	AY401209 Pan trogl
10	777	44.3	2671	9 AY406144	AY406144 Pan trogl
11	708	40.3	782	6 CD353576	CD353576 UI-M-GMO-
12	579	33.0	711	7 CN409312	CN409312 170004243
13	531.2	30.3	653	1 AU296039	AU296039 AU296039
14	503	28.7	1484	3 CR717163	CR717163 Tetraodon
15	497.2	28.3	582	5 BP359939	BP359939 BP359939
16	477.8	27.2	1051	9 CN5047PP	CN5047PP Tetraodon
17	449.8	25.6	787	4 BT732193	BT732193 603352796
18	440.6	25.1	608	4 BM490671	BM490671 ppp2n.pk0
19	416.2	23.7	1101	9 CN504XAU	CN504XAU Tetraodon
20	414.4	23.6	678	5 BU205182	BU205182 604156686
21	385	21.9	795	7 CN460548	CN460548 UI-M-HB0-
22	380	21.7	702	7 CK314839	CK314839 SB0204082
23	368.6	21.0	772	5 BX873944	BX873944 BX873944
24	367	20.9	679	5 BM964289	BM964289 UI-M-EQ0-

25	350.8	20.0	723	6 CA344834	CA344834 675311 NC
26	346	19.7	973	4 B1827857	B1827857 603074065
27	344.8	19.6	732	6 CD609655	CD609655 56040124H
28	341.8	19.5	941	2 BE779818	BE779818 601465317
29	340.8	19.4	872	9 CNS02JYV	AL200851 Tetraodon
30	334.4	19.1	895	4 BG261524	BG261524 602373277
31	328.6	18.7	808	5 BU292395	BU292395 603604634
c	324	18.5	839	9 CNS028BY	AL185767 Tetraodon
33	322.2	18.4	1078	9 CNS054KQ	AL320867 Tetraodon
34	316.6	18.0	777	5 BU456417	BU456417 603217533
c	315.2	18.0	943	9 CNS058KW	AL326057 Tetraodon
36	312.6	17.8	666	9 CE724887	CE724887 tigr-gss-
37	311.2	17.7	373	2 BE207131	BE207131 ball609.y
38	303.6	17.3	907	9 CNS04HBU	AL290739 Tetraodon
39	302.2	17.2	2182	3 AK034263	AK034263 Mus muscu
c	301.6	17.2	554	4 BM681239	BM681239 UI-B-EJ0-
41	294.4	16.8	521	7 CN468842	CN468842 hh Ab Bra
42	290.4	16.5	633	6 CB517356	CB517356 seal1gb53
43	285.6	16.3	600	4 BG806878	BG806878 2042-42 M
44	284.8	16.2	2007	3 BC022720	BC022720 Mus muscu
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ALIGNMENTS

RESULT 1	AK038395	3675 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK038395				
DEFINITION	Mus musculus adult male hypothalamus cDNA, RIKEN full-length RECEPTOR 8 PRECURSOR, full insert product.				
ACCESSION	AK038395				
VERSION	AK038395.1	GI:26086504			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research				

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BC051384 3693 bp mRNA linear HTC 19-NOV-2003
 Mus musculus glutamate receptor, metabotropic 8, mRNA (cDNA clone
 IMAGE:6466902), containing frame-shift errors.
 BC051384
 BC051384.1 GI:30410848
 HTC.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3693)

Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Urdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 22388257
 PUBLISHED 12477932
 2 (bases 1 to 3693)
 Strausberg, R.
 Direct Submission
 Submitted (25-APR-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgi.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)

Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov

Blakesley, R.W., Bouffard, G.G., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Akter, N., Ayele, K., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McLooney, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAK Plate: 100 Row: j Column: 8
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 6680104
 This clone has the following problem: frame shifted.

FEATURES

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 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 47.9%; Score 841.4; DB 3; Length 3693;
 Best Local Similarity 69.6%; Pred. No. 2e-184;
 Matches 1155; Conservative 0; Mismatches 501; Indels 3; Gaps 1;
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 Db 1390 GGGTTTGGACCATCTTTAGAGCGGAATCTTGGCAATAATCGAAGAAATGTGTGTTT 1449
 QY 103 GCCGAGTTCTCGGAGGACAACTTCCATTCGAAGTTGAGCGCGCACGCGCTCAAGAGGGA 162
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 Db 1807 AACACAAAAGTACAGAAATACAAATCATCGGCCACTGGACCAATCACTTCACTCAAAA 1866
 QY 523 ATAGAGCGGATGCAAGTGGCCAGGGAGTGGCGAGAGTGGCGCGCTCCACTTGCAGTCTG 582
 Db 1867 GTGGAAGACATGCAAGTGGGCTTAATAGAGAGACACAGCCACCCAGCATCTGTCTGCGACCTG 1926
 QY 583 CCCTCCAGCCCGGGGAGCGAAGAGACTGTGAGGCGATGGCTTGTCTGCTGGCAGCTGC 642
 Db 1927 CCGTCAAGCCCTGGGGAGAGAAACCCGTGAAAGGGGTCCTTGTCTGCTGGCACTGT 1986

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Qy 703 GACATCGCGGCCACAGAGAACCGACGAGCTGCCAGCCCATCCCCATCGTCAAGTTGGAG 762
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Qy 763 TGGGACTCGCGTGGCGGTGCTGCECTCTTCCTGCGCGGTGGTGGGATCGCGCCACG 822
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DEFINITION genomic survey sequence.
ACCESSION AY401210
VERSION AY401210.1 GI:39757199
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2748)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2748)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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QY 939 CCTCATGATCGCAGAGCCGAGCTGGGAGCTGTGCTGCTCGCGCATCTCTCAGGCT 998
Db 1932 CTAATGATGCGAGCCAGATGTGCGAGTGTCTTCCGACGTGCTCTTGGGTT 1991
QY 999 CGGATGAGCATCAGTACCGGCGCTGTGACCAAGACCAACCGCATTTACCGATCTT 1058
Db 1992 GGGTATGTGTATGATGAGCGCCCTTTTAAACAAAACCAATCGGATTTACGATAT 2051
QY 1059 TGACAGGGCAACGGTGGTCACTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCGGCTG 1118
Db 2052 CGAGCAGGGCAAGAAATCGTGACAGCTCCAGACTCATAGACCCCAACATCAAACTGC 2111
QY 1119 CATCACCTTCATCTCATCTCCTGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG 1178
Db 2112 AATTACCTCAGTTAATATCGGTGCACTTTAGGTGCTTTATTTGGTTTGGGTTGA 2171
QY 1179 CCCCTCCCACTCGGTGGTGGACTTCCAGGACCAAGCACTTGACCCCGCTTTGCCAG 1238
Db 2172 CCCACCAACATCATATAGACTACGATGAAATGAACCAACCAAGCAAGCCAG 2231
QY 1239 GGGCGTCTCAAGTGGGACATCTCGGACCTGTCCCTCATCTGCTGCTGGGCTACAGAT 1298
Db 2232 GGGAGTCTCAAAATGTGACATCACAGACCTTCAGATCAATTTGTTCTTTGGGATATAGCAT 2291
QY 1299 GCTGCTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1358
Db 2292 TCTTCTCATGTTCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2351
QY 1359 CAAAGGAGCCAAAGCCCATCGGCTTCCACATGTATACCACTGCTGCTGCTGCTGCTGCT 1418
Db 2352 TAATGAAGCCAAAGCCCATCGGATTCATATGTATACAGCTTGTATGCTATGCTGCTT 2411
QY 1419 CATCCCATCTTTTGGACCTTCAGTACAGCCGAGAGCTGTATCATCCAGAACCCAC 1478
Db 2412 CATCCCAATATTTTGGCAGAGCCGCAATCAGCAGAAAAGCTCTACATACAAACCCAC 2471
QY 1479 ACTGAGCGTCTCGGTGAGTCTGAGCGCTTCAGTGTCCCTGGGGAGTCTTACATGCCAA 1538
Db 2472 GCTTAAATCTCCATGAACCTAAGTGTGATCAGTGGCGCTGGGGATGCTATATGCCGAA 2531

QY 1539 AGTCTACATCATCTCTTCCACCCGAGCAGAACCTGCGCAAGCGCAGCTCTCAA 1598
Db 2532 AGTGTACATCATCTCTTCCACCCGAGCAGAACCTGCGCAAGCGCAGCTCTCAA 2591
QY 1599 AGCCGTGGTTCACCGCGCCAGCAGCTGTCACAAAGTTCACACAGAAGGGCACTTCAGGCG 1658
Db 2592 GGCCGTAGTTCACAGCAGCAGCAGCTGTCATCGAGGCTGTTCACACAAACCCAGTGCAGGCG 2651
QY 1659 CAATGGGAAGCAAAATCAGAGCTGTGTGAGAACCTGGAGACCCAGCAGCTGCTGCTACCA 1718
Db 2652 CAATGGTGGGCAAGAGCAGAACTTTGTGAAATGTAGACCCCAAGCAGCCTGCTGCTGCA 2711
QY 1719 ACAGACCTACCTACCTACCTACCAACCAATGCCATCTA 1754
Db 2712 AAAGAAGTATGTGCTTATTAACCTGCTTATCTA 2747

RESULT 4
BC034118 3399 bp mRNA linear HTC 19-NOV-2003
LOCUS
DEFINITION Mus musculus glutamate receptor, metabotropic 6, mRNA (cDNA clone IMAGE:4511841), containing frame-shift errors.

ACCESSION BC034118
VERSION BC034118.1 GI:21706621
KEYWORDS HTC.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3399)
AUTHORS Klausner, R.D., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Leach, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, I.B., Toshlyuk, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fane, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalek, U., Smaluk, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE
PUBMED 22388257
2 (bases 1 to 3399)

REFERENCE Direct Submission
AUTHORS Strausberg, R.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: The Capko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 44 Row: i Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
 This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:4511841"
 /tissue_type="Eye, retina, mouse strain C57Bl/6"
 /clone_lib="NIH MGC_94"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

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Query Match      46.9%; Score 822.6; DB 3; Length 3399;
Best Local Similarity 70.2%; Pred. No. 4.6e-180;
Matches 1121; Conservative 0; Mismatches 467; Indels 9; Gaps 1;

Qy 43 GGGTTTCAGCCGATCTTCTCCAGCGCGCACGCTGGACAAACAGCGCGCAACATCTGGTTT 102
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 103 GCGGAGTTCTGGAGGACAACTTCATTCGAAGTTGAGCCGCGCAGCGCTCAAGAGGGA 162
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 221 GCTGAGTTCTGGAGAGAGATTTTAACTGCAAACTTAACCACTCAGTGGGCGCAGTCAGAT 280
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 163 AGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGGCAGGACTCGGCTATGAGCAG 222
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 281 GATTCACCCGGAATGACAGGCGAGGAACGATCGGCCAGGACTCACCTATGAACAG 340
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 223 GAGGGAAGTGCAGTTCTGATGACGCTGTGTACGCCATGTGGCCAGCGCGCTGCACGCC 282
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 341 GAGGGAAGTGCAGTTCTGATAGATGCTGTGTATGCCATCGCTCATGCTCTGCACAGC 400
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 283 ATGCACCGTAGCTGTGTCGCGCGGTAGAGACTTCGCTCGGATGGAGCCCGTGGAT 342
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 401 ATGCACCAAGCACTTCGCCAGGCGCACACAGGTCTGTGCCAGCGCATGGAGCCTACTGAT 460
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 343 GGCACCCAGCTGCTTAAGTACATCAGGAACGTCACCTTCTCAGGCATTCGCGGGAACCT 402
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 461 GCGCGGAACCTTGCTGCATATCCGAGCAGTCCGCTTCAATGTAGCGCAGGAACCCCA 520
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 403 GTAACTTTCAATGAGAACGAGACGCAACCGGGGCGCTACGACATCTACAGTACCAACTG 462
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 571 GTGATGTTCAATGAGAAATGGGGATGCCCGCGGGCGCTATGACATCTTCCAGTACCAAGCA 580
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 463 CGCAATG-----GTCGCGCGAGTACAAAGTTCATCGGCTGTGGACACAGCACTG 513
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 574 TGCAGTCTGCCCTGCGACCGCGGAGCGAAGAGACTGTGAAGGGCATGGCTTGTGTC 633
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 761 TGGCACTGTGAGGCCCTGCGACCGGTACCGCTTCCAGTGGAGCGAGTTTACCGTGTGAGGCC 820
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 694 TGCCCTTACGACATCGCGGCCACAGAACCGCAGAGCTGCCAGCCATCCCATCGTC 753
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 821 TGTCCAGGGACATAGACCCGACACCCCAACCACTGGCTGCCGTCCCACTCCCGTGGTG 880
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 754 AAGTTGGAGTGGGACTCGCCGCTGGGCGGTGTGTCGCCCTTCTTCTGGCGGTGGTGGCATC 813
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 881 CGCTGACCTGGTCTCTCCGTGGCGCGCTCTGCCCTTCTCTCTGGGTGTCCTTGGGCATC 940
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Db 941 ATGSCCAACCAACAATCAATGCTACCTTATGGAACACACGACACTCCCATAGTCCGC 1000
Qy 874 GCCTTCGGGCGGGAACATGAGCTACGCTGCTGTGGCGGCGATCTTTCTGTGTACGCCACT 933
Db 1001 GCCTTCGGGCGTGAAGCTTAGCTATGCTGTCTACCGGCTATCTTCTGTATCTACGCCATC 1060
Qy 934 ACCTTCCTCATGATCGCAGAGCGGACCTGCGGAGCTGTGTGCTCGCGCGCATCTTCTCTA 993
Db 1061 ACCTTCCTCATGATGAGCGGCTTGTGCGACCGCTTGTGCTTCCCGAAGACTCTTGTGTC 1120
Qy 994 GGGCTCGGCATGAGCATCAGCTACGCGGCCCTGCTGACCAAGACCAACCGCATTTACCGC 1053
Db 1121 GGCTTGGGTACCGCTCAGCTACTCTGCCCTGTCTACCAAGACCAACCGCATCTACCGC 1180
Qy 1054 ATCTTTGAGCAGGGAACAGGTCCGTGCTGCTGCCCGGCTTTTCATCAGCCCGGCTCGCAG 1113
Db 1181 ATTTTCGAGCAAGGAAGCGCTCTGTCAAGCGGCCACCTTTCATCAGCCCGCATCGCAG 1240
Qy 1114 CTGSCCATCACTTCTCATCTCCCTGAGAGTGTCTCGGCATCTCGGATCTGGGTGTGGTG 1173
Db 1241 CTAGTCATCACTTTCGGCTTACCTCCCTGCGAGTGTGGAGTGTAGCGTGTGGGG 1300
Qy 1174 GTGGACCCCTCCCACTCGGTGTGGACTTCCAGGACCAACGACACTTGACCCCGCTTT 1233
Db 1301 GCCACACTTCCACAGCGGTGATGATATGAGGAACAGAGGACGGTGGACCTTGAGCAA 1360
Qy 1234 GCCAGGCGGTGCTCAAGTGCACATCTCGGACCTGCTCCCTCATCTGCTGCTGGGTAC 1293
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Qy 1294 AGCATGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1353
Db 1421 AGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1480
Qy 1354 ACCTTCAACGAGGCGCAAGCCATCGGCTTCAACATGTACACCATCTGCTGCTGCTGCTG 1413
Db 1481 ACCTTCAATGAAGCAAGCCATCGGCTTCAACATGTACACCATCTGCTGCTGCTGCTGCTG 1540
Qy 1414 GCCTTCACTCCCATCTTTTGGCACTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCT 1473
Db 1541 GCCTTTCGCTCCCATCTTTTGGCACTCTTTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1600
Qy 1474 ACCACATGAGGCTCTCGGTGAGTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAG 1533
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Qy 1534 CCCTAAGTCTACATCATCTCTTCCACCGGAGCAGAACGTCGCCAAGCGCAAGCGCAGT 1593
Db 1661 CCCTAAGTCTACATCATCTCTTCCATCCAGAGCAGAACGTCGAGAGCGGAGGCGAGC 1720
Qy 1594 CTCAAGCGGTGCTCAGCGCGCCACCATGTCTCAACA 1630
Db 1721 CTCAAGAGACCTCCAGATGGCGGCCCGCCCAAGA 1757

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RESULT 5

AV401208
 LOCUS
 DEFINITION Homo sapiens GRM7 gene, VIRTUAL TRANSCRIPT, partial sequence,
 Genomic survey sequence.
 ACCESSION AV401208
 VERSION AV401208.1 GI:39757197
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2748)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

RESULT 6	AY406145	2667 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	Mus musculus GRM8 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION					
ACCESSION	AY406145				
VERSION	AY406145.1	GI:39762119			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarial,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2667)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarial,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
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ORIGIN	Query Match 45.9%; Score 806.2; DB 9; Length 2667;				
	Best Local Similarity 69.2%; Pred. No. 2.8e-176;				
	Matches 1148; Conservative 0; Mismatches 498; Indels 13; Gaps 3;				
Qy	43	GGGTTGCGACCGATCTTCTCCAGCGCGACGCTGGACAAACAGCGCGAATCTGGTTT	102		
Db	1018	GGGTTTGACCGATCTTTAGAGCGGAACTCTTGCCAAATATCGAAGAAATGTGTGTTT	1077		
Qy	103	GCGGAGTTCTGGAGGACAACTTCCATTTGCAAGTTGAGCGCGCACGCGTCAAGAGGGA	162		
Db	1078	GCAGAAATTTGGGAGGAGAAATTTGGATGCAAAATTTAGGATCAGATGGG---AAGAGGAAC	1134		
Qy	163	AGCCACATCAGAACTGCACCAACCGAGAGCGCATCGGGCAGGACTCGGCTATGAGCAG	222		
Db	1135	AGTCATATAAGAAATGCAAGGCGTGGAGCGAAATTTGACGGGATTCATTTACGAAACA	1194		
Qy	223	GAGGGAAGGTGCAGTTTCGTGATTTGACGCTGTGTACGCGATGGGCGACGCGCTGCACGCC	282		
Db	1195	GAAGGAAGGTTCAATTTGTATTTATGATGATGATGATGATGATGATGATGATGATGATG	1254		
Qy	283	ATGACCCGCTGACCTGTGTCCCGCGCGTAGGACTCTGCCCTCGCATGGACCCCGTGGAT	342		
Db	1255	ATGCACAAAGAACTCTGCGCTCGTTTACATAGGCGCTTTGCCAAGGATGGTTACCATCGAT	1314		
Qy	343	GGCACCAGCTGTTAAGTATCATCAGGAACGTCACCTTCTCAGGCGATTTGCGGGGACCCCT	402		
Db	1315	GGGAAGAGCTACTCTGGGTTTACATCAGGCGCGTGAATTTTAAATGGCAGCGCTGGTACACT	1374		
Qy	403	GTAACCTTCAATGAGAACGGAGACGCGACCGCGGCGCTACGACATCTTACAGTACCAACTG	462		
Db					
Db	1375	GTCACTTTTAAATGAGAAATGAGATGCTCCGGGACGCTACGATATCTTCCAAATATCAGATA	1434		
Qy	463	CGCAATGGCTCGGCGGAGTACAAGGTCAATCGGCTCGTGGACAGACCACTCGACCTCAGA	522		
Db	1435	AACAAACAAAGTACAGAAATACAAATCATCGGCACATGGACCAATCAACTTCAC-----	1488		
Qy	523	ATAGAGCGGATGCAAGTGGCCAGGGAGTGGCCAGCAGCTGCGCGCTCCATCTCGAGTCTG	582		
Db	1489	GTGGAAGACATGCACTGGGCTAATAGAGAGACACAGCACCCAGCATCTGTCTGAGCGCTG	1548		
Qy	583	CCCTGCCAGCCCGGGAGCGAAGAGACACTGTGAGGGCATGGCTTCTGCTGCGCACTGC	642		
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Qy	643	GAGCCCTGCACCGGTTACCAAGTACCAAGTGCACCGCTACACCTGTGAAGACTCGCCCTAC	702		
Db	1609	GAACGCTGCGAGGGTTATACTACAGGTGAGACGAATCTCTCTGTGAATCTTGCCTTTTG	1668		
Qy	703	GACATGCGGCGCCACAGAGAACCGCAGAGCTGCCAGCCCATCCCATCGTCAAGTTGGAG	762		
Db	1669	GATCAGAGACCAACATCAACCGCAGCTGGCTGCCAGAGGATTCCTCATCATCAAGTTGGAG	1728		
Qy	763	TGGGACTCGCGTGGGCGGCTGTGCCCCCTCTTCTGCGCGTGGTGGGCGATCGCGCGCACG	822		
Db	1729	TGGCATTCACCTCGGCGGCTGTACCTGTGTTCATAGCAATATTTGGGAATCATTTGCCACC	1788		
Qy	823	CTGTTCTGTGTGTGTCAGTTTGTGCGCTACAACGATACCCCATCGTCAAGGCGCTCGGGC	882		
Db	1789	ACCTTTGTGATTTGTGACCTTTTGTCCGCTATATGACACCAATCTGTGAGAGCTTCTGGG	1848		
Qy	883	CGGGAATCTGAGCTACGCTGCTGGCGGGCATCTTTCTGTGTACGCGCATCTTCTCTC	942		
Db	1849	CGGGAATCTAGTTATGTGCTCTAAACGGGATTTTCTCTGTACTCAATCACATTTTGTG	1908		
Qy	943	ATGATCGCAGAGCGGACCTGTGGGACCTGTTCGCTCGCGCGCATCTTCTTAGGCTCGGC	1002		
Db	1909	ATGATTCGGGACCTGACAAATCATCTGCTCTTTCCGAAGGATCTTCTCGGAGCTTGGT	1968		
Qy	1003	ATGAGCATCAGCTACGCGGCGCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAG	1062		
Db	1969	ATGTGTTTCACTATGACGACCTTTTGACCAAAACAAACCGTATCCACCGAATATTCGAG	2028		
Qy	1063	CAGGCAAAACGGTCTGCTGAGTCCCGCGCTTTCATCAGCCCGGCTCGCAGCTGGCCATC	1122		
Db	2029	CAAGGGAAGAAATCTGTACAGCACCTAAGTTTCATCAGCCAGCATCCAGCTGGTGATC	2088		
Qy	1123	ACCTTCATCTCATCTCCCTGCGAGCTGCTCGGCATCTGCGTGTGTTGCTGGTGGACCCC	1182		
Db	2089	ACCTTCAGCCTCATCTCCGTACAGCTCCTTTGGAGTGTTTGTGTGGATTCCTGCTGGATCCC	2148		
Qy	1183	TCCCACTCGTGTGGGACTTCCAGGACCAACGGACACTTGACCCCGCTTTTGGCAGGGGC	1242		
Db	2149	CCCCACACCATCATTTGATGATGAGAAACAGGAACACTGGATCCCGAGAACCGCAGGGGA	2208		
Qy	1243	GTGCTCAAGTGCAGACATCTCGGACCTGTCCCTCATCTGCTGCTGGGCTACAGCATGCTG	1302		
Db	2209	GTGCTCAAGTGTGACATTTCCGATCTGTCACTCATTTGTTTCACTGGGATACAGTATCCTC	2268		
Qy	1303	CTGATGTGTACGTGTACTGTGTACGCCCATCAAGACCCGAGCGGTGCCCGAGACCTTCAAC	1362		
Db	2269	CTGATGTGTACTTGTACTTGTATGCCATTAACACAGAGGGGTTCAGAAACGTTTCAAT	2328		
Qy	1363	GAGGCCAAGCCCATCGGCTTCCACCATGTACACCACTGCAATGTCTCTGGCTGGGCTTCATC	1422		
Db	2329	GAAGCCAAACCTATTTGGAATTTACCATGTACACCACTGTGCATCATTTGGTTAGCTTTCAAT	2388		
Qy	1423	CCCATCTTTTGGCAGCTCAGCTCAGCCGCAAGCTGTATCATTCAGACAAACCACTG	1482		
Db	2389	CCCATCTTTTGGTACAGCCAGCTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2444		
Qy	1483	ACGCTCTCCGTGAGCTGTAGCGCTTACGTGTCCCTGGGGATGCTCTACATGCCCAAGTC	1542		
Db	2445	ACTGTCTCCATGAGTTTAAAGTGTCTTCTCTGGGAATGCTCTATATGCCAAAGTT	2504		

QY 1543 TACATCATCTCTTCCACCGGAGCAGAGCTGCCCAAGCGCAGCTCTCAAGCC 1602
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 DB 2505 TATATTATAATTTTCATCCAGAGCAGAAAGCTTCAAAAAACGCAAGAGAAAGCTTCAAGGCT 2564
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 QY 1603 GTGGTCAACCGCCGACCATGTCCTCAACAGTTTCACACAGAGGGCAACTTTCAGGCCCAAT 1662
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 |||||
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 DB 2625 GCGGAGGTGAAAGTGAAGTCTGTGAGAGTCTTGAAGACC 2663
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RESULT 7

AY406143 2671 bp DNA linear GSS 15-DBC-2003
 Locus
 DEFINITION Homo sapiens GRM8 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY406143

VERSION AY406143.1 GI:39762117

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2671)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D., and Cargill, M.

Infering nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

JOURNAL

PUBMED

REFERENCE 2 (bases 1 to 2671)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D., and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

FEATURES

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LOCUS
DEFINITION
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ACCESSION
AK053447.1 GI:26343462
VERSION
AK053447.1
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PubMed
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PubMed
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PubMed
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
MEDLINE
11076861
5
The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
NATURE 420, 563-573 (2002)
6 (bases 1 to 4209)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hitamoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
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DEFINITION Pan troglodytes GRM7 gene, VIRTUAL TRANSCRIPT, partial sequence,
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VERSION AY401209.1 GI:39757198
KEYWORDS GSS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2611)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITILE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2611)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITILE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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ORIGIN

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment

FEATURES

source

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QY      824  TGTTCGTGGTGGTCAAGTTTGTGGCTACACGATACCCCATCGTCAAGGCTCGGGCC 883
DB      1790  CTTTGTGTAGTGAACCTTTGTCCGCTATAATGACACACCTATCGTAGGGCTTCAGSAC 1849

QY      884  GGGAACTGAGCTACGCTGCTGCTGGCGGCGATCTTTCTGTGTGCTACGCGACTACTCTCTCA 943
DB      1850  GCGAACTTAGTTACGCTGCTCTTAACGGGGATTTTCTCTGTATTCAATCAGGTTTTTAA 1909

QY      944  TGATCGCAGAGCCGACCTGGGGACCTGTTGCTCCGCGCATCTTCTTAGGGCTCGGCA 1003
DB      1910  TGATTCGAGCACCAGATACATATATGCTCTTCCGCGGATCTTCTTAGGACTGGCA 1969

QY      1004  TGAGCATCAGCTACGCGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGC 1063
DB      1970  TGTGTTTTCAGCTATGACGCGCTTTCGACCAAAACCGATATCACCAGAAATATTGAGC 2029

QY      1064  AGGGCAAAACGGTCCGTCAGTGCCCGCGTTTCATCAGCCCGCGCTCGCAGCTGGCCATCA 1123
DB      2030  AGGGGAAGAAATCTGTACAGCGCCCAAGTTTATTTAGTCCAGCATCTCAGCTGGTATCA 2089

QY      1124  CTTTCATCTCATCTCTCGCTGAGCTGCTGGGATCTGGGATCTGGTGTGGTGGACCCCT 1183
DB      2090  CTTTCAGCTCATCTCTCGCTGAGCTCTTGGAGTGTGTTGCTGTGTTGTTGGATCCCC 2149

QY      1184  CCCACTCGTGGTGGACTTCCAGGACCAACGACACTTGGACCCCGCTTTGCCAGGGCG 1243
DB      2150  CCCACATCATCTTCACTATGGAGAGCAGCGACACTAGATCCAGAGAGGCGCAGGGAG 2209

QY      1244  TGCTCAAGTCGGACATCTCGGACCTGCTCCATCTGCTGCTGGCTACAGCATGCTGCG 1303
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QY      1304  TGATGTCACGCTGACTGTGACGCATCAAGACCCGAGGCGTGGCCGAGACTTTCACACG 1363
DB      2270  TGATGTCACGCTGACTGTTATGTCATTAAACGAGAGGTGCTCCAGAGACTTTTCAATG 2329

QY      1364  AGGCAAGCCCATCGGCTTCCAGTGTACACCACTGATGCTGTGCTGGCTGGCTTCATCC 1423
DB      2330  AAGCAAAACCTATTGGATTTACCATGTATACCCATGTATCCACCTGCATCATTTGGTTAGCTTCATCC 2389

QY      1424  CCATCTTTTGGCACTCAGAGTCAGCGCGCAGCTGACAGTCCAGCAAGCTGTACATCCAGCAACCACTGA 1483
DB      2390  CCATCTTTTGGTACAGCCAGTCCAGCAAGAAAGNNNNNNNNNNNNNNNNNNNNNNNN 2449

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QY      1544  ACATCATCTCTTCCACCGGAGCAGAGTGGCCCAAGCGCAGCGAGTCTCAAGCGCG 1603
DB      2510  ATATTATTAATTTTTCATCCAGAACAGAAATGTTTCAAAAACGCAAGAGGAGCTTCAAGGCTG 2569

QY      1604  TGGTCACCGCGCCACCATGTCCAAAGTTTCAACAGAGGCAACTTTCAGGCCCAATG 1663
DB      2570  TGGTGACAGCTGCCACCATGCAAGCAAACTGATCCAAAAGAGAAATGACAGACCAATG 2629

QY      1664  GGGAGGCAAAATCAGAGCTGTGTGAGAACCTGGAGACC 1701
DB      2630  GCGAAGTGAAAGTGAAGTCTGTGAGAGTCTTGAAACC 2667

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RESULT 11

CD353576

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CD353576 782 bp mRNA linear EST 15-JUL-2003
UI-M-GW0-cgc-a-23-0-UI.r1 NIH_BMAP_GW0 Mus musculus cDNA clone
IMAGE:30360694 5', mRNA sequence.

CD353576
CD353576.1 GI:31146077
EST.

Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 782)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.
 Location/Qualifiers
 1. 782
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30360694"
 /tissue_type="whole brain"
 /dev_stage="1, 5 and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_GMO"
 /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 40.3%; Score 708; DB 6; Length 782;
 Best Local Similarity 94.0%; Pred. No. 1.5e-153; Indels 0; Gaps 0;
 Matches 735; Conservative 0; Mismatches 47;
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 1 CCCTGGCGTGTGCTGCCCTCTTCTGCGTGTGGGCATTGCTGCCACGCTGTTCGTG 60
 832 GTGGTCAGCTTTGTGGCTACAAAGATACCCCAATCGTCAAGGCTCGGGCGGGAATG 891
 61 GTGGTCACCTTTGTGGCTACAAAGATACCCCAATCGTCAAGGCTCGGGCGGGAATG 120
 892 AGCTACGTCGCTGGCGGATCTTCTGCTGCTAGCCATCTACCTTCTCATATCGCA 951
 121 AGCTACGTCGCTGGCGGATCTTCTGCTGCTATGCCACCTTCTCATATCGCA 180
 952 GAGCGGACCTGGGACCTGTTCGCTCGCGCGCATCTTCTTAGGCTCGGCATGAGCATC 1011
 181 GAGCTGACCTGGGACCTGTTCCTCTCGCGCATCTTCTTAGGCTGGGCATGAGCATC 240
 1012 AGCTACGCGGCTGCTGACCAAGACCAACCGCATTTACCGCATTTTGAGCAGGGCAAA 1071
 241 AGCTACGCGGCTGCTGACCAAGACCAACCGCATTTACCGCATTTTGAGCAGGGCAAG 300
 1072 CGGTGGTCACTGGCGGCTTCTATCAGCGGCTCGAGCTGGCCATCACCTTCATC 1131
 301 CGGTGGTCACTGGCGGCTTCTATCAGCGGCTCGAGCTGGCCATCACCTTCATC 360
 1132 CTCACTCTCCCTGACGCTGCTGGCATCTGCGTGTGTTCTGCTGGAGACCCCTCCCACTCG 1191

Db 361 CTCACTCTCCCTGACGCTGCTTGGCATCTGCGTGTGTTCTGCTGGAGCCCTCCCACTCG 420
 Qy 1192 GTGTGTGACTTCCAGGACCAACGACACTTGGACCCCGCTTTGGCAGGGCGTCTCAAG 1251
 Db 421 GTGTGTGACTTCCAGGACCAACGACACTTGGACCCCGCTTTGGCAGGGCGTCTCAAG 480
 Qy 1252 TGGGACATCTCGGAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
 Db 481 TGTGACATCTCGGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 Qy 1312 ACGTGTACTGTGTACGACATCAAGACCCGAGGCGTGGCCGAGACCTTCAAGAGGCCAAG 1371
 Db 541 ACGTGTACTGTGTATGCCATCAAGACTCGAGGCGTGGCTGAGACCTTCAATGAGGCCAAG 600
 Qy 1372 CCCATCGGCTTCCACCTGTACACCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1431
 Db 601 CCCATCGGCTTCCACCTGTACACCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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 Db 661 TTTGGCACCTCGCAGTGGCTGACAGCTGTACATCCAGACCAACACACTGACCGTCTCT 720
 Qy 1492 GTGAGTCTGAGCGCTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
 Db 721 GTGAGTCTGAGCGCTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Qy 1552 CT 1553
 Db 781 CT 782

RESULT 12

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 LOCUS 17000424346609 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
 DEFINITION
 ACCESSION CN409312
 VERSION CN409312.1 GI:47396436
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 711)
 AUTHORS Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 TITLE Transcription characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
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FEATURES

Location/Qualifiers
 1. 711
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
 /clone_lib="GRN_ES"
 /note="Poligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 33.0%; Score 579; DB 7; Length 711;
 Best Local Similarity 91.1%; Pred. No. 1.4e-123;
 Matches 637; Conservative 0; Mismatches 60; Indels 2; Gaps 2;

QY 1093 TTCATCAGCCCGCCTCGCAGCTGGCCATCACCTTCATCCTCATCTCCTCGAGCTGTC 1152
Db |||||
301 TTCATCAGCCCGCCTCACAGCTGGCCATCACCTTCAGCCTCATCTCGCTGAGCTGCTG 360
QY 1153 GGCATCTGGTGTGGTTCTGGTGGACCCCTCCCACTCGGTGGTGGACTTCAGGACCA 1212
Db |||||
361 GGCATCTGGTGTGGTTCTGGTGGACCCCTCCCACTCGGTGGTGGACTTCAGGACCA 420
QY 1213 CGGACACTTGACCCCGCTTTGCCAGGGCGTGTCTCAAGTGGGACATCTCGGACCTGTCC 1272
Db |||||
421 CGGACACTGACCCCGCTTCCGAGGGGTGTCTCAAGTGTGACATCTCGGACCTGTCC 480
QY 1273 CTCATCTGCTGTGGGCTACAGCATGTGCTGTGATGGTCAAGTGTGATGTAAGCCATC 1332
Db |||||
481 CTCATCTGCTGTGGGCTACAGCATGTGCTCATGCTCACGTGCACCGTGTATGCCATC 540
QY 1333 AAGACCGAGGGGTGCCGAGACCTTCACAGGCGCCAGCCC 1374
Db |||||
541 AAGACCGGGGTGCCGAGACCTTCATATGAGGCCAGCCC 582

Search completed: June 21, 2005, 08:50:49
Job time : 5991 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 04:25:23 ; Search time 314 Seconds
(without alignments)
9145.432 Million cell updates/sec

Title: US-10-828-332-6
Perfect score: 1755
Sequence: 1 atgcaggggtatcatc.....acaccaaccatgcatctag 1755

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1712.4	97.6	4095	5	PCT-US91-09422-18
2	1707.6	97.3	2838	4	US-09-820-809-1
3	1516.4	86.4	2426	5	PCT-US91-09422-20
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5	1470.8	83.8	3431	3	US-09-641-318-3
6	1470.8	83.8	3884	4	US-09-016-434-1074
7	1470.8	83.8	3884	4	US-09-820-809-14
8	1467.8	83.6	2736	3	US-08-617-785-1
9	1467.8	83.6	2736	4	US-08-617-785-1
10	880.6	50.2	2961	2	US-08-407-875-1
11	880.6	50.2	2961	3	US-09-277-858-1
12	871	49.6	2670	3	US-09-126-280-1
13	860.2	49.0	2635	3	US-09-126-280-3
14	839	47.8	3321	3	US-08-855-146-1
15	839	47.8	3321	3	US-08-855-146-3
16	823.8	46.9	2724	3	US-08-823-110-5
17	823.8	46.9	2724	3	US-08-604-298-5
18	823.8	46.9	3833	3	US-08-823-110-2
19	823.8	46.9	3833	3	US-08-604-298-2
20	821.6	46.8	2997	1	US-08-453-862-1
21	821.6	46.8	2997	2	US-08-452-734A-1
22	821.6	46.8	2997	3	US-08-176-401B-1
23	821.6	46.8	2997	5	PCT-US94-14989-1
24	808.8	46.1	3021	4	US-09-016-434-1118
25	806.8	46.0	2745	3	US-08-617-785-11
26	806.8	46.0	2745	3	US-08-617-785-11
27	793.4	45.2	2766	3	US-08-617-785-13

28 793.4 45.2 2766 4 US-09-817-464-13
29 793.4 45.2 3804 3 US-08-617-785-3
30 793.4 45.2 3804 4 US-09-817-464-3
31 680 38.7 1588 3 US-08-617-785-7
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33 350.6 20.0 630 3 US-08-617-785-15
34 350.6 20.0 630 4 US-09-817-464-15
35 350 19.9 2619 3 US-08-337-797A-1
36 350 19.9 2619 3 US-08-337-797A-3
37 350 19.9 2619 3 US-09-258-523-1
38 350 19.9 2619 3 US-09-258-523-3
39 345.2 19.7 2621 4 US-09-016-434-1490
40 293.4 16.7 2637 3 US-08-794-158-1
41 293.4 16.7 2637 3 US-08-794-158-3
42 293.4 16.7 3410 4 US-09-016-434-1080
43 290.2 16.5 3919 1 US-08-072-574-5
44 290.2 16.5 3919 1 US-08-486-270-5
45 290.2 16.5 3919 3 US-08-367-264-5

ALIGNMENTS

RESULT 1
PCT-US91-09422-18
; Sequence 18, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,806
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-6PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4095 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:

Sequence 13, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1490, Ap
Sequence 1, Appl
Sequence 3, Appl
Sequence 1080, Ap
Sequence 5, Appl
Sequence 5, Appl

US-09-820-809-1

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Query Match      97.3%; Score 1707.6; DB 4; Length 2838;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 4; Indels 0;
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Qy	102	TGCGGAGTCTTGGGAGGACAACATTCCAATTCGCAAGTTGAGCGCCACACGCGCTCAAGAGGG	161
Db	290	TGCGGAGTCTTGGGAGGACAACATTCCAATTCGCAAGTTGAGCGCCACACGCGCTCAAGAGGG	349
Qy	162	AAGCCACATCAAGAAGTGCAACCAACGAGAGCGCATCGGGCAGGACTTCGGCCTATGAGCA	221
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Db	470	CATGCACCGTAGCCTGTGTCTGGCCCGTAGAGACTCTGCCCTCGCATGACACCCCGTGA	529
Qy	342	TGGCACCACAGCTGCTTAAGTACATCAGGAACGTCACACTTCTCAGGGCAATTCGGGGGAACCC	401
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Qy	402	TGTAACTTCATGAGAAACGAGACGCAACGCGGGCGCTACGACATCTACAGTACCAACT	461
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Qy	462	GCGCAATGGCTCGSCCAGTACAAGGTCAATCGGCTCGTGGACAGACCACTCGACACCTCAG	521
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Qy	522	AATAGAGCGATGCACTGGCGAAGAGTGGCCAGCAGCTGCGCGCTCCATCTGCACTCT	581
Db	710	AATAGAGCGATGCACTGGCGAAGAGTGGCCAGCAGCTGCGCGCTCCATCTGCACTCT	769
Qy	582	GCCTCGCACCGGGAGCGAAGAGACTGTGAGGGCATCGCTGCTGCTGGGCACCTG	641
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Db	830	CGAGCCCTGCACCGGGTACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCCCTA	889
Qy	702	CGACATCGGCCCNACAGAGAACCGCACGAGCTGCAGCCCATCCCATTCGTCAAGTTGGA	761
Db	890	CGACATCGGCCCNACAGAGAACCGCACGAGCTGCAGCCCATCCCATTCGTCAAGTTGGA	949
Qy	762	GTGGGACTCGCCGTGGGCCGTGCTGCCCTCTTCTTGGCCGTGGTGGGCATCGCGCCAC	821
Db	950	GTGGGACTCGCCGTGGGCCGTGCTGCCCTCTTCTTGGCCGTGGTGGGCATCGCGCCAC	1009
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Qy	882	CCGGGAATGAGCTACGTGCTGTGGCGGGGCACTTCTGTGCTACGCCACTACTTCCT	941
Db	1070	CCGGGAGCTAGCTACGTGCTGTGGCGGGGCACTTCTGTGCTACGCCACTACTTCCT	1129
Qy	942	CATGATCGCAGACCCGACCTGGGGACCTGTTCTGCTCCGCGCATCTTCCTAGGGCTCGG	1001
Db	1130	CATGATCGCAGACCCGACCTGGGGACCTGTTCTGCTCCGCGCATCTTCCTAGGGCTCGG	1189
Qy	1002	CATGAGCATCAGCTACGCGGCCCTGTGTGAACAAGACCAACCGCATTTACCGCATCTTTGA	1061
Db	1190	CATGAGCATCAGCTACGCGGCCCTGTGTGAACAAGACCAACCGCATTTACCGCATCTTTGA	1249

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RESULT 3
PCT-US91-09422-20
; Sequence 20, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; CURRENT APPLICATION DATA:
; Version #1.25

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APPLICATION NUMBER: PCT/US91/09422
FILING DATE: 19911212
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,007
FILING DATE: 18-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,481
FILING DATE: 30-JAN-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/626,806
FILING DATE: 12-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-6PC
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: SR13
PCT-US91-09422-20

Query Match 86.4%; Score 1516.4; DB 5; Length 2426;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 42 AGGTTTCAGCCGATATCTTCAGCCGACGCTGGACAAACAGCGCCAACTCTGGTT 101
Db 738 AGGGTTCAGCCGATATCTTCAGCCGACGCTGGACAAACAGCGCCAACTCTGGTT 797

Qy 102 TCCGAGTCTGGGAGGCACTTCATTGCAAGTTGAGCGCCACCGGCTCAAGAGGG 161
Db 798 TGCCGAGTCTGGGAGGCACTTCATTGCAAGTTGAGCGCCACCGGCTCAAGAGGG 857

Qy 162 AAGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCA 221
Db 858 AAGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGAGCA 917

Qy 222 GGAGGGGAAGTGCAGTTGTTGATGAGCGCTGTGTACGCCATGGGCCACGCGCTGCAGC 281
Db 918 GGAGGGGAAGTGCAGTTGTTGATGAGCGCTGTGTACGCCATGGGCCACGCGCTGCAGC 977

Qy 282 CATGCACCGTGACCTGTGTCCGCGCGGTAGGACTCTGCCCTCGCATGGACCCGCTGGA 341
Db 978 CATGCACCGTGACCTGTGTCCGCGCGGTAGGACTCTGCCCTCGCATGGACCCGCTGGA 1037

Qy 342 TGGCACCCAGCTGCTTAAGTATACATCAGGAACGTCAACTTCTCAGGCATTTGGGGGAACC 401
Db 1038 TGGCACCCAGCTGCTTAAGTATACATCAGGAACGTCAACTTCTCAGGCATTTGGGGGAACC 1097

Qy 402 TGTAACCTTCAATGAGAACGAGACGCAACCGGGCGCTACGACATCTACAGTACCAACT 461
Db 1098 TGTAACCTTCAATGAGAACGAGACGCAACCGGGCGCTACGACATCTACAGTACCAACT 1157

Qy 462 GGGCAATCGCTCGGCGGAGTACAGGTATCGGCTCGTGAGACACACCTGCACCTCAG 521
Db 1158 GGGCAATCGCTCGGCGGAGTACAGGTATCGGCTCGTGAGACACACCTGCACCTCAG 1217

Qy 522 AATAGACGGATGAGTGCAGGAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT 581
Db 1218 AATAGACGGATGAGTGCAGGAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT 1277

Qy 582 GCCCTGCCAGCCCGGGGAGCGAAAGAGACTGTGAAGGGCATGTGCTGCTGCGCACTG 641
Db 1278 GCCCTGCCAGCCCGGGGAGCGAAAGAGACTGTGAAGGGCATGTGCTGCTGCGCACTG 1337

Qy 642 CGAGCCCTGCACCGGGTACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCCCTA 701
Db 1338 CGAGCCCTGCACCGGGTACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCCCTA 1397

Qy 702 CGACATCGGCCCCACAGAGAACCGACAGCTGCGACCCATCCCATCTGTCAGTTGGA 761
Db 1398 CGACATCGGCCCCACAGAGAACCGACAGCTGCGACCCATCCCATCTGTCAGTTGGA 1457

Qy 762 GTGGGACTCGCGGTGGGCGGTGCTGCGCCCTTCTTGGCGGTGGTGGGATCGCGGCCAC 821
Db 1458 GTGGGACTCGCGGTGGGCGGTGCTGCGCCCTTCTTGGCGGTGGTGGGATCGCGGCCAC 1517

Qy 822 GCTGTTCTGCTGCTCACGTTTGTGCGCTACAAAGATACCCCATCTGTCAGAGGCTCGGG 881
Db 1518 GCTGTTCTGCTGCTCACGTTTGTGCGCTACAAAGATACCCCATCTGTCAGAGGCTCGGG 1577

Qy 882 CCGGAACTGAGCTACGCTGCTGCTGCGGGGATCTTCTGTGCTACGCACTACCTTCCT 941
Db 1578 CCGGAGCTGAGCTACGCTGCTGCTGCGGGGATCTTCTGTGCTACGCACTACCTTCCT 1637

Qy 942 CATGATCGAGAGCGGACCTGGGACCTGTTGCTCGCGGATCTTCTTAGGCTCGG 1001
Db 1638 CATGATCGAGAGCGGACCTGGGAGCTGTTGCTCGCGGATCTTCTTAGGCTCGG 1697

Qy 1002 CATGAGCATCAGCTACGCGGCCCTGTGTAACCAAGCAACCGCATTTACCGCATCTTGA 1061
Db 1698 CATGAGCATCAGCTACGCGGCCCTGTGTAACCAAGCAACCGCATTTACCGCATCTTGA 1757

Qy 1062 GCAGGGCAACCGGTGCTGAGTGCCTGCGGTTTCAATCAGCCCGGCTCGAGCTGGCCAT 1121
Db 1758 GCAGGGCAACCGGTGCTGAGTGCCTGCGGTTTCAATCAGCCCGGCTCGAGCTGGCCAT 1817

Qy 1122 CACCTTCATCTCATCTCCCTGACGCTGCTGGGATCTGCGGTGTTGTTGTTGGGACCC 1181
Db 1818 CACCTTCATCTCATCTCCCTGACGCTGCTGGGATCTGCGGTGTTGTTGTTGGGACCC 1877

Qy 1182 CTCCCATCTCGGTGTTGAGCTTCCAGAGCAACCGGACACTTGAACCCCGCTTTGCGAGGG 1241
Db 1878 CTCCCATCTCGGTGTTGAGCTTCCAGAGCAACCGGACACTTGAACCCCGCTTTGCGAGGG 1937

Qy 1242 CGTCTCAAGTGCACATCTCGGACCTGCTGCTCATCTGCTGCTGCGGCTACAGCATGCT 1301
Db 1938 CGTCTCAAGTGCACATCTCGGACCTGCTGCTCATCTGCTGCTGCGGCTACAGCATGCT 1997

Qy 1302 GCTGATGCTCAAGTGTACTGTGTACGCGCATCAACCGGCGCTGCCGAGACCTTCAA 1361
Db 1998 GCTGATGCTCAAGTGTACTGTGTACGCGCATCAACCGGCGCTGCCGAGACCTTCAA 2057

Qy 1362 CGAGGCCAAGCCCATCGGCTTACCATGTACCAACCTGCAATTTGCTGGCTGGCTTCAT 1421
Db 2058 CGAGGCCAAGCCCATCGGCTTACCATGTACCAACCTGCAATTTGCTGGCTGGCTTCAT 2117

Qy 1422 CCCCATCTTTTGGCACTCAAGTGCAGCGCAAGCTGTATCATTCAGACAAACCACT 1481
Db 2118 CCCCATCTTTTGGCACTCAAGTGCAGCGCAAGCTGTATCATTCAGACAAACCACT 2177

Qy 1482 GACGGTCTCGGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGATGCTTACATGCCCAAGT 1541
Db 2178 GACGGTCTCGGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGATGCTTACATGCCCAAGT 2237

Qy 1542 CTACATCATCTCTTCCA 1559
Db 2238 CTACATCATCTCTTCCA 2255

RESULT 4
US-09-641-318-1
; Sequence 1, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU

TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
AND RELATED NUCLEIC ACID COMPOUNDS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: ELI LILLY AND COMPANY

STREET: LILLY CORPORATE CENTER

CITY: INDIANAPOLIS

STATE: INDIANA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/641,318

FILING DATE: 18-Aug-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/816,178A

FILING DATE: 12-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: GAYLO, PAUL J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10579

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-0756

TELEX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3431 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 26..2761

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-641-318-1

Query Match 83.8%; Score 1470.8; DB 3; Length 3431;

Best Local Similarity 91.1%; Pred. No. 0;

Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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DB 1051 AGGCTTCAGCCGCTACTTCTCCAGCGCGACGCTGACACAAACCGCGCAACATCTGGTT 1110

QY 102 TGCCGAGTTCTGGGAGGCAACTTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAAGGG 161

DB 1111 TGCCGAGTTCTGGGAGGCAACTTCCACTGCAAGCTGAGCCGCCACGCGCTCAAGAAGGG 1170

QY 162 AAGCACATCAAGAGTGACCAACAGGAGGCGATCGGGGAGGACTCGGCCCTATGAGCA 221

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QY 402 TGTAACCTTCATGAGACGGAGCGCACCGGGCGCTACGACATCTACCACTACCAACT 461

DB 1411 TGTAACCTTCATGAGATGGAGATGCGCGCTTGGCGCTATGACATCTACCAATACCACT 1470

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DB 1771 GTGGGCTCGCCGCTGGGCGGCTGCTGCCCTCTTCTGCGCGGTGGGATCGCGCCAC 1830

QY 822 GCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881

DB 1831 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1890

QY 882 CCGGGAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941

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DB 1951 CATGATCGCAGAGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2010

QY 1002 CATGAGCATCAGCTACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1061

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DB 2071 GCAGGCAAGCGTCCGCTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2130

QY 1122 CACCTTCATCTCATCTCCCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181

DB 2131 CACCTTCAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2190

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DB 2191 CTCCACCTCGTGTGGACTTCCAGGACCAACGAGCACTTGAACCCCGCTTGGCAGGGG 2250

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QY 1302 GCTGATGTGCT 1361

DB 2311 GCTCATGTGCT 2370

QY 1362 CGAGGCCAAGCCCATTCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421

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DB 2431 CCCCATCTTTTGGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2490

QY 1482 GACGCTCTCCGCT 1541

DB 2491 GACGCTCTCCGCT 2550

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Db 2551 CTACATCATCTCTTCCACCCGGAGCAAGCGTGCCTCAAGCGCAAGCGCCTCAAAGC 2610
Qy 1602 CGTGTACCGCGCCGACCATGTCCAAAGTTTACACAGAGGCGCAACTTCAGGCCCAA 1661
Db 2611 CGTGTACCGCGCCGACCATGTCCAAAGTTTACACAGAGGCGCAACTTCAGGCCCAA 2670
Qy 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAGAACTGTGAGACCCAGCGCTGGCTACCAACA 1721
Db 2671 CGGAGAGCCCAAGTCTGAGCTCTGCGAAGACTTGGAGCCCGAGCGCTGGCCACCAACA 2730
Qy 1722 GACCTACGTCACTACACCAACCATGCGCATCTAG 1755
Db 2731 GACTTACGTCACTTACACCAACCATGCAATCTAG 2764

RESULT 5

US-09-641-318-3
; Sequence 3, Application US/09641318
; Patent No. 6384205
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; WU, SU
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; AND RELATED NUCLEIC ACID COMPOUNDS

; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELI LILLY AND COMPANY
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: INDIANA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 46285

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,318
; FILING DATE: 18-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,178A
; FILING DATE: 12-MAR-1997

; ATTORNEY/AGENT INFORMATION:
; NAME: GAYLO, PAUL J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10579
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-641-318-3
Query Match 83.8%; Score 1470.8; DB 3; Length 3431;
Best Local Similarity 74.2%; Pred. No. 0;
Matches 1271; Conservative 291; Mismatches 152; Indels 0; Gaps 0;

Qy 42 AGGTTTCACCGGATATCTTCACCGCGCAGCGTGGACAAACAGCGGCGCAATCTGGTT 101
Db 1051 AGGCUUCGACCGCUAUUCUCAGCGCGCAGCGUGGACAAACAGCGGCGCAACUCGGUU 1110
Qy 102 TGCCAGATTTCGGAGGAGCAACTTCATTGCAAGTTGAGCGGCCACCGCGCTCAAGAAGGG 161
Db 1111 UGCCGAGUUCUGGGAGGAGCAUUCACUGCAAGCUGAGCGGCCCAAGAGGG 1170

Qy 162 AAGCCACATCAAGAAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCGCTATGAGCA 221
Db 1171 CAGCCACGUCUAAGAAGUGCACCAACCGUGAGCGAAUUGGCGAGUATCAGCUUAUGAGCA 1230
Qy 222 GGAGGGGAAGGTGAGTTCGTGATTGACGCTGTGTACGCCATCGGCCACCGGCTGCAGCG 281
Db 1231 GGAGGGGAAGGUGCAGUUGUUGAUCGAGUGCGUGUACGCCAUGGGGCCACGCGCUGCAGCG 1290
Qy 282 CATGCAACGCTGACCTGCTCCCGSCCGGTAGGACTCTGCGCTCGCATGGAACCCCGTGA 341
Db 1291 CAUGCAACGUGACCGUGUCCCGGCGCGUGGGGUCUCGCGCGCAUGGACCCUGUAGA 1350
Qy 342 TGGCACCCAGCTGCTTAAGTACATCAGGAAAGTCAACTTCTCAGGCAATTCGGGGAAACCC 401
Db 1351 UGGCACCCAGCUGCUUAAGUACAUCCGAAAGCUCUUCUCAGGCAUCGCGAGGAAACCC 1410
Qy 402 TGTAACCTTCAATGAGAAACGGAGAGCGCACCGGGGGCGCTACGACATCTACCAATGTAACCACT 461
Db 1411 UGUGACCUCAUAGAGAAUGGAGUAGCGCCUGGGCGCUUAGCAUCAUCCAAUACCAAGCU 1470
Qy 462 GCGCAATGGCTCGGCGCAGTACAAAGTTCATCGGCTCGTGACACAGACACCACTGCACTCAG 521
Db 1471 GCGCAACAUUCUGCCGAGUACAAAGUUAUUGGUCUCUGAGACACCAUCCUGCACTUUG 1530
Qy 522 AATAGACGGATGCAAGTGGCCAGGGAGTGCCAGAGCTGCGCGCTCCATCTCGAGTCT 581
Db 1531 AAUAGAGCGGAUGCAGCUGGCGCGGAGCGGAGCAGCAGCUGCCCGCUCUAGCAGCUCU 1590
Qy 582 GCCCTGCAGCCCGGGAGCGAAAGAAAGTGTGAAGGGCATGSGCTTGTGCTGGCACTG 641
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Db 1651 CGAGCCUUGCACAGGGUACAGUACACAGGUGGACCGCUACACCUUAGAGCGUUCUCCUA 1710
Qy 702 CGACATCGCGGCCACAGAGAACCGCACAGCTGCGAGCCATCCCATCGTCAAGTTGGA 761
Db 1711 UGACAUGCGGCCACACAGAGAACCGCACGGGCGCGGCCCAUCCCAUCAUCAAGCUUGA 1770
Qy 762 GTGGGACTCGCGGTGGGCGGTGTCGCCCTCTTCTGCGCGTGTGGGCGATCGCGCGCAC 821
Db 1771 GUGGGGCGCGCCCGGCGCGGCGCUCUUCGCGCGGUGGUGGCAUCGCGCGCAC 1830
Qy 822 GCTGTTCTGCTGCTGCTCACGTTTGTGCGCTACAAAGTACACCGCATCGTCAAGGCGCTCGGG 881
Db 1831 GUUUGUCGUGGUGAUCACUUUGUCCGCUACAGACACAGCCCAUCCGCAAGGCGCUGGG 1890
Qy 882 CCGGGAATGAGCTACGCTGCTGCTGCGGGGATCTTTCTGTGTACGCGCACTACTCTTCT 941
Db 1891 CCGUGAACUGAGCUACGUGCUGCGGCGAGGCAUCUUCUGUGCUAUGGCCACCAUUCUUC 1950
Qy 942 CATGATCGAGAGCGGACCTGGGACCTGTTGCTCGCGCGCATCTTCTTAGGGCTCGG 1001
Db 1951 CAUGAUCGUGAGCGCGACCTUGGCGCACCGCUGCGCGCGGCAUUCUUCUGGAGCUAGG 2010
Qy 1002 CATGAGCATCAGCTACGCGCGCTGTGACCAAGACCAACCGCATTTTACCGCATCTTTGA 1061
Db 2011 GAUGAGCAUCAGCUAUGAGCCUUGCUCACCAAGACCAACCGCAUACUACCGCAUUCUGCA 2070
Qy 1062 GCAGGGCAAAAGGTCGGTCAAGTGCCTCGCGGCTTTTCATCAGCCCGCGCTCGCAGCTGGCGAT 1121
Db 2071 GCAGGGCAAGCGUGGUGCAGUGGCCCAACGCUUUAUUCAGCGCCCGCCUACACAGCUGGCCAU 2130
Qy 1122 CACTTTCATCTCTCTCCCTGAGCTGCTCGGATCTGCGTGTGGTGTGGTGGGACCC 1181
Db 2131 CACCUAGCCUACUUCGUGCUGGAGGCGUGGCGAUCUGUGUGUGUGUGUGUGUGGUGGAGCC 2190
Qy 1182 CTCCCACTCGGTGCTGACTTTCAGAGGACCAAGACACTTTGACCCCGCTTTCGAGGGG 1241
Db 2191 CUCCACUCCGUGUGUGAUCUUCAGAGACCAAGCGGACACUAGACCCCGCGUCCGCGAGGG 2250
Qy 1242 CGTCTCAAGTGCAGCATCTCGGACCTGTCCCTCATCTGCTGTGGGCTACAGATGCT 1301

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Db 2251 UGUGCUAAGUGAUAUCUGGACCGGCUAUCUGGCGGCUAUCUGGCGGCUAUCAGCAUGCU 2310
Qy 1302 GCTGATGCTCAGCTGTACTGTGTACCGCCATCAAGACCCGAGGCGTGCAGGACCTTCAA 1361
Db 2311 GCUAUGGUCACGUGACCGUAGUAGCAUAGACACGCGGCGUGCGGCGGACCUCAU 2370
Qy 1362 CGAGGCAAGCCATCGGCTTACCATGTACACCACTGCTGTGTGTGTGTGTGTGTGTGTGT 1421
Db 2371 UGAGGCCAAGCCCAUUGGCUUACCAUGUACACCAUUGCAUGGUGUGGCGGCUUACAU 2430
Qy 1422 CCCCATCTTTTGGCACCTTCAGTCCAGCCGACAGCTGTATCATCCACACACCACT 1481
Db 2431 CCCCACUUCUUGGACCGGCUAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2490
Qy 1482 GACGGTCTCCGCTGAGTCTGAGGCGCTTCACTGTCTCTGCGGATGCTTACATGCCCAAGT 1541
Db 2491 GACGGUCUGGUGAGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2550
Qy 1542 CTACATCATCTCTTCCACCGGAGCAGAACTGTGCGGCAAGCGGAGCGGAGCTTCAAAGC 1601
Db 2551 CUACAUCUCCUUCUACCCGAGCAGAACTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2610
Qy 1602 CGTGTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1661
Db 2611 CGUGGUAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2670
Qy 1662 TGGGGAAGCAAAATCAGAGCTGTGTGAGAACTGTGAGACCCGAGCGGCTTCAAGCA 1721
Db 2671 CGAGAGGCAAGUGUGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2730
Qy 1722 GACCTACGTCACCTACCAACCACTGCCATCTAG 1755
Db 2731 GACUACGUCACUACCAACCAUGCAUCUAG 2764
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RESULT 6

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US-09-016-434-1074
; Sequence 1074, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
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; INFORMATION FOR SEQ ID NO: 1074:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3884 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: g1160182

US-09-016-434-1074

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Query Match 83.8%; Score 1470.8; DB 4; Length 3884;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Qy 42 AGGGTTTCACACCGATATCTTCTCCAGCGCGCACCGCTGACAAACAGCGCGCAACATCTGGTT 101
Db 1196 AGGCTTCACACCGTACTTCTCCAGCGCGCACCGCTGACAAACAGCGCGCGCAACATCTGGTT 1255
Qy 102 TGCCAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAAGG 161
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Qy 522 AATAGAGCGGATGCAATGCGGAGTGGCCAGAGCTGCGCGCGCTCCATCTGCACTCT 581
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Db 1916 GTGGGAGCTGCGGCGGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGG 1975
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Db 1976 GCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2035
Qy 882 CCGGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 941
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Db	2036	CCGTGAACCTGAGCTACTGCTGTCTGGCAGGCATCTTCTCTGTCTATGCCACCACTTCCT	2095
Qy	942	CATGATCGCAGAGCCGACCTGGGGACCTGTGTGGCTCCGGCGCATCTTCTAGGGCTCGG	1001
Db	2096	CATGATCGCTGAGCCGACCTTGGCACCTGCTCGCTGCGCCGAATCTTCTGGGACTAGG	2155
Qy	1002	CATGAGCATCAGCTACCGGGCCCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGA	1061
Db	2156	GATGAGCATCAGCTATGACGCCCTGCTTCACCAAGACCAACCGCATCTTACCGCATCTTCGA	2215
Qy	1062	GCAGGGCAACCGTTCGCTCAGTGCCCGCGTTTCATCAGCCGCGCTTCGCAGCTGGCCAT	1121
Db	2216	GCAGGGCAAGCGTTCGCTCAGTGCCCGCACGCTTCATCAGCCCGCTTCACAGTGGCCAT	2275
Qy	1122	CACCTTCATCCTCATCTCCCTGCAGCTGCTCGGCATCTGCGTGTGGTTCTGTGTGACCC	1181
Db	2276	CACCTTCAGCTCATCTCGCTGCAGCTGCTGGGCATCTGTGTGTGGTTTGTGGTGGACCC	2335
Qy	1182	CTCCCACTCGGTGGTGACTTCCAGGACCAACGGACACTTGCACCCCGCTTTCGCCAGGG	1241
Db	2336	CTCCCACTCGGTGGTGACTTCCAGGACCAACGGAGACACTGCACCCCGCTTTCGCCAGGG	2395
Qy	1242	CGTGCTCAAGTGCACACTCTCGGACCTGTGCCCTCATCTGCGTCTGTGGGCTACAGCATGCT	1301
Db	2396	TGTGCTCAAGTGCACACTCTCGGACCTGTGCTCATCTGCTGCTGTGGCTACAGCATGCT	2455
Qy	1302	GCTGATGGTCACTGTACTGTGTACGGCANTCAAGACCGAGGGGTGCCGAGACCTTCAA	1361
Db	2456	GCTCATGGTCACTGTGACCGGTGTATGCCATCAAGACACGGGGGTGCCGAGACCTTCAA	2515
Qy	1362	CGAGGCCAAGCCCATCGGCTTCCACATGTACACCACTGCATTTGCTGTGGCTGGGCTTCAT	1421
Db	2516	TGAGGCCAAGCCCATTTGGCTTCCACATGTACACCACTTGCATCGTCTGGCTGGGCTTCAT	2575
Qy	1422	CCCACATCTTTTGGCACCTCAAGTCAAGCCGACAAAGTGTACATCCAGACAAACCACT	1481
Db	2576	CCCACATCTTTTGGCACCTCGCAGTGGGCCGACAAGCTGTATCATCCAGACGACGAGCT	2635
Qy	1482	GACGGTCTCGGTGAGTCTGAGCGCTTCAGTGTCCCTGGGGATGCTCTACATGCCCAAAGT	1541
Db	2636	GACGGTCTCGGTGAGTCTGAGCGCTCGGTGTCCCTGGGAATGCTCTACATGCCCAAAGT	2695
Qy	1542	CTACATCATCTCTTCCACCCGGAGCAGACGTGCCAACCGCAAGCGCATGCTCTCAAAGC	1601
Db	2696	CTACATCATCTCTTCCACCCGGAGCAGACGTGCCAACCGCAAGCGCATGCTCTCAAAGC	2755
Qy	1602	CGTGGTCAACGCCCGCACCATGTCTCAACAGTTTCAACAGAGGGGAACCTTCAGGCCCAA	1661
Db	2756	CGTGGTCAACGCCCGCACCATGTCTCAACAGTTTCAACAGAGGGGAACCTTCAGGCCCAA	2815
Qy	1662	TGGGGGAAGCCAAATCAGAGCTGTGTGAGAACCTGGAGACCCCGACGCTGGCTACCAACA	1721
Db	2816	CGGAGAGCCCAAGTCTGAGTCTTCGAGAACCTTGAGGCCCGACGCTGGCCACCAACA	2875
Qy	1722	GACCTAGCTCACTTACACCAACCATGCAATCTAG	1755
Db	2876	GACTTACGTCACCTTACCAACCAACCATGCAATCTAG	2909

RESULT 7

US-09-820-809-14
 Sequence 14, Application US/09820809
 Patent No. 6608176
 GENERAL INFORMATION:
 APPLICANT: CHAUDHARI, NIRUPA
 APPLICANT: ROPER, STEPHEN D.
 TITLE OF INVENTION: TASTE RECEPTOR FOR UMAMI (MONOSODIUM GLUTAMATE) TASTE
 FILE REFERENCE: 70373/275576
 CURRENT APPLICATION NUMBER: US/09/820,809
 CURRENT FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: 60/193,454
 PRIOR FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 14									
; LENGTH: 3884									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-820-809-14									
Query Match 83.8%; Score 1470.8; DB 4; Length 3884;									
Best Local Similarity 91.1%; Pred. No. 0;									
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;									
Qy	42	AGGGTTGCACCGATACTTCTCCAGCCGACAGCTGGACAAACACAGCGGCAACATCTGGTT	101						
Db	1196	AGGCTTCGACCGGTACTTCTCCAGCCGACAGCTGGACAAACACCGCGCAACATCTGGTT	1255						
Qy	102	TGCCGAGTTCCTGGAGAGCAACTTCCATTGCAAGTTGAGCGCGACACGCTCAAGAAGGG	161						
Db	1256	TGCCGAGTTCCTGGAGAGCAACTTCCATTGCAAGCTGAGCGCGCACGCCCTCAAGAAGGG	1315						
Qy	162	AAGCCACATCAAGAAGTGACCAACCGAGAGCGCATCGGCGAGGATTCGCGCTTATGAGCA	221						
Db	1316	CAGCCACGTCAAGAAGTGACCAACCGTAGCGAAATTGGGACGATTCAGCTTATGAGCA	1375						
Qy	222	GGAGGGGAAGGTGCGATTCTGTGATTGACGCTGTGTAGCCATGGGCGACCGGCTGCACGC	281						
Db	1376	GGAGGGGAAGGTGCGATTCTGTGATTGATGATGCGGTGTACGCCATGGGCGACCGCTGCACGC	1435						
Qy	282	CATGCAACGCTGACTGTGTCTCCGGCCGCTAGGACTCTGCCCCTCGCATGGACCCCGTGA	341						
Db	1436	CATGCAACGCTGACTGTGTCTCCGGCCGCTGAGGGCTCTGCCCAGGATGGACCTGTAGA	1495						
Qy	342	TGGCACCCAGCTGCTTAAAGTACATCAGGAACGTCAACTTCTCAGGCAATTGCGGGGAACCC	401						
Db	1496	TGGCACCCAGCTGCTTAAAGTACATCAGGAACGTCAACTTCTCAGGCAATCGAGGGAACCC	1555						
Qy	402	TGTAACTTCAATGAGAAACGAGACGCAACCGGGGCGCTACGACATCTACAGGTACCAACT	461						
Db	1556	TGTGACCTTCAATGAGAAATGAGATGCGCTGGGCGCTATGACATCTACCAATACCACT	1615						
Qy	462	GGCAATGGCTCGGCGAGTACAAAGGTCTATCGGCTCGTGGACAGACACCTGCACCTCAG	521						
Db	1616	GGCAACGATTCGCGAGTACAAAGGTCTATGGCTCTGTGACGTGACACCTGCACCTTAG	1675						
Qy	522	AATAGACGGATGCAGTGGCCAGGGAGTGCCACAGCAGCTGCCCGCTCCATCTGCAGTCT	581						
Db	1676	AATAGACGGATGCAGTGGCCGGGAGCGGGCAGCAGCTGCCCGCTCCATCTGCAGCT	1735						
Qy	582	GCCTTGCACCCCGGGAGCGAAAGACTGTGAAGGCAATGGCTTGTCTGGGCACTG	641						
Db	1736	GCCCTGCAACCGGCTGAGCGGAAGAAGCAGTGAAGGGCATGCCCTTGTCTGGGCACTG	1795						
Qy	642	CGAGCCTGCACCGGGTACCAGTACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCTTA	701						
Db	1796	CGAGCCTTGCACAGGGTACCAAGTACAGTGGACCGCTACACCTGTGAAGACGTGCCCTTA	1855						
Qy	702	CGACATCGCGGCCACAGAGAACCGCAGCTGCCAGCCCATCCCCATCGTCAAGTTGGA	761						
Db	1856	TGACATCGGCGCCACAGAGAACCGCAGCGGCTGCCGCGCCATCCCCATCATCAAGCTTGA	1915						
Qy	762	GTGGGACTCGCGGTGGGCGGTGCTGCCCTCTTCTTGGCGGTGGTGGGCAATCGCGCCAC	821						
Db	1916	GTGGGCTCGCCCTGGGCGGTGCTGCCCTCTTCTTGGCGGTGGTGGGCAATCGCTGCAC	1975						
Qy	822	GCTGTTCGTGGTGCAGTTTGTGGCTACAGATACCCCATCGTCAAGGCTCGGG	881						
Db	1976	GTTGTTCGTGGTGCATCACTTTGTGGCTACAGACACGCCCATCGTCAAGGCTCGGG	2035						
Qy	882	CCGGAACTGAGTACGTGTCTGTGGCGGCACTTTTCTGTGTAGCCCACTACCTTCCT	941						
Db	2036	CCGTGAATGAGCTACGTGTCTGTGGCAGGCACTTCTCTGTGTATGCCCACTTCCT	2095						
Qy	942	CATGATCGCAGACCGCACTGGGACCTGTTCTGCTCGCGCGCATCTTCTAGGGCTCGG	1001						

Db 2096 CATGATCGTGAAGCCGACCTTGGACCTGCTGCTGCCCGCAATCTTCTGGACTAGG 2155
Qy 1002 CATGAGCATCAGCTAGCGGCGCTGCTGACCAAGACCAACCCGATTTACCGCATTTTGA 1061
Db 2156 GATGAGCATCAGCTAGCGGCGCTGCTACCAAGACCAACCCGATTTACCGCATTTTGA 2215
Qy 1062 CGAGGGCAACGGTGGTCAAGTCCCGGCTTTCATCAGCCGGGCTCGAGCTGGCAT 1121
Db 2216 CGAGGGCAAGCGCTGGTCAAGTCCCGGCTTTCATCAGCCGGGCTCGAGCTGGCAT 2275
Qy 1122 CACCTTCATCTCATCTCCCTCGAGCTGCTCGGCTCTGCTGCTGCTGCTGCTGCTGCT 1181
Db 2276 CACCTTCAGCTCATCTCGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2335
Qy 1182 CTCCCATCTGGTGGTACTTCCAGAACCAACGACACTTGAACCCCGCTTTGCCAGGG 1241
Db 2336 CTCCCATCTGGTGGTACTTCCAGAACCAACGACACTTGAACCCCGCTTTGCCAGGG 2395
Qy 1242 CTGCTCAAGTGGACATCTCGACCTGCTCCCTCATCTGCTGCTGCTGCTGCTGCTGCT 1301
Db 2396 TGTGCTCAAGTGGACATCTCGACCTGCTCCCTCATCTGCTGCTGCTGCTGCTGCTGCT 2455
Qy 1302 GCTGATGGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1361
Db 2456 GCTCATGCTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2515
Qy 1362 CGAGGCCAAGCCCATCTGGCTTCCACCATGATACCACTGATGCTGCTGCTGCTGCTGCT 1421
Db 2516 TGAGGCCAAGCCCATCTGGCTTCCACCATGATACCACTGATGCTGCTGCTGCTGCTGCT 2575
Qy 1422 CCCCATCTTTTGGACCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1481
Db 2576 CCCCATCTTTTGGACCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2635
Qy 1482 GACGCTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1541
Db 2636 GACGCTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2695
Qy 1542 CTACATCATCTCTTCCACCGGAGCAGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601
Db 2696 CTACATCATCTCTTCCACCGGAGCAGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2755
Qy 1602 CGTGTACCGCGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1661
Db 2756 CGTGTGTACCGCGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2815
Qy 1662 TGGGAGGCAATCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1721
Db 2816 CGGAGAGGCAATCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2875
Qy 1722 GACCTACGTCACCTACCAACCATGCCATCTAG 1755
Db 2876 GACTTACGTCATACCAACCATGCAATCTAG 2909

RESULT 8
US-08-617-785-1
; Sequence 1, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Rainer
; APPLICANT: Lindauer, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7

; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2736)
US-08-617-785-1

Query Match 83.6%; Score 1467.8; DB 3; Length 2736;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1559; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
Qy 42 AGGGTTCCACCGATATCTTCTCAGCCGCGACCTGGACAAACAGCGCGCAACATCTGGTT 101
Db 1036 AGGCTTCAGCCGCTACTTCTCAGCCGCGACCTGGACAAACAGCGCGCAACATCTGGTT 1085
Qy 102 TGCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGCGCCACCGCTCAAGAAGGG 161
Db 1086 TGCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGCGCCACCGCTCAAGAAGGG 1145
Qy 162 AAGCCACATCAAGAAGTGACCAACCGAGAGCGCATCGGCGAGGACTCGGCCCTATGAGCA 221
Db 1146 CAGCCACGTCAGAAGTGACCAACCGTGAGCGAATTCGGCAGGATTCAGCTTATGAGCA 1205
Qy 222 GGAGGGGAAGTGTCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 281
Db 1206 GGAGGGGAAGTGTCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1265
Qy 282 CATGCACCGTCACTGCTGCTCCGCGGTAGGACTCTGCTCGCATGCGACCCCGTGA 341
Db 1266 CATGCACCGTCACTGCTGCTCCGCGGTAGGACTCTGCTCGCATGCGACCCCGTGA 1325
Qy 342 TGGCACCAGCTGCTTAAGTACATCAGGAACGTCAACTTCTCAGGCATTCGGGGAAACC 401
Db 1326 TGGCACCAGCTGCTTAAGTACATCAGGAACGTCAACTTCTCAGGCATTCGGGGAAACC 1385
Qy 402 TGTAACTTCAATGAGAACGAGACGACCGGGGGCTACGACATCTACCAGTACCACT 461
Db 1386 TGTGACCTTCAATGAGAACGAGACGACCGGGGGCTACGACATCTACCAGTACCACT 1445
Qy 462 GCGCAATGGCTCGGCGGAGTCAAGGTTCATCGGCTCGTGGGAGACACCTGCACTCAG 521
Db 1446 GCGCAATGGCTCGGCGGAGTCAAGGTTCATCGGCTCGTGGGAGACACCTGCACTCAG 1505
Qy 522 AATAGAGCGGATGAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGAGTCT 581
Db 1506 AATAGAGCGGATGAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGAGTCT 1565
Qy 582 GCCCTGCGAGCCCGGGAGCGAAAGACCTGTGAGGGGCTATGGCTTGTCTGGGACTG 641
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Qy 642 CGAGCCCTGCAACCGGTTACCAAGTGGACCGCTACACCTGTAGAGCTGCGCCCTA 701
Db 1626 CGAGCCCTGCAACCGGTTACCAAGTGGACCGCTACACCTGTAGAGCTGCGCCCTA 1685
Qy 702 CGCATGCGGCGCCACAGAGAACCGCAGAGCTGCGCAGCCCATCCCATCTGCAAGTTGA 761
Db 1686 TGACATGCGGCGCCACAGAGAACCGCAGAGCTGCGCAGCCCATCCCATCTGCAAGTTGA 1745
Qy 762 GTGGAGCTGCGCGGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 821
Db 1746 GTGGAGCTGCGCGGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1805
Qy 822 GCTGTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 881
Db 1806 GCTGTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1865

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QY 882 CCGGAACTGAGTACGTGCTGGCGGCATCTTTCTGTGCTACGCACCTACCTTCCT 941
Db |||
QY 1866 CCGTGAATGAGTACGTGCTGGCAGGATCTTCTGTGCTATGACACACCTTCCT 1925
Db |||
QY 942 CATGATCGAGACCGGACCTGGGACCTGTTCGCTCCGCCGATCTTTCCTAGGGCTGG 1001
Db |||
QY 1936 CATGATCGTGGCGCCGACCTGGCACCTGCTCGCTGGCGGAACTTTCCTGGGACTAGG 1985
QY 1002 CATGAGCATCAGTACGGCGGCTGCTGACCAAGACCAACCGCATTTACCGCATTTTGA 1061
Db |||
QY 1986 GATGAGCATCAGTATGAGCGCTGCTCACCAGACCAACCGCATCTACCGCATCTTGA 2045
QY 1062 CGAGGCAAAAGCTCGGTGAGTGGCCCGCTTTTCATCAGCCCGCTCGCAGCTGGCCAT 1121
Db |||
QY 2046 CGAGGCAAGCGCTCGGTGAGTGGCCCGCTTTTCATCAGCCCGCTCGCAGCTGGCCAT 2105
QY 1122 CACCTTCATCTCATCTCCCTGCACTGCTCGGCATCTCGCTGTGGTTCGTGGTGGACCC 1181
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QY 2106 CACCTTCAGCTCATCTCGCTGCAGCTGCTGGGCATCTGTGTGTTTGTGTGGACCC 2165
QY 1182 CTCACATCGGTGAGTCTTCAGGACCAACGGACACTTGAACCCCGCTTTGCCAGGG 1241
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QY 2166 CTCACATCGGTGAGTCTTCAGGACCAACGGACACTTGAACCCCGCTTTGCCAGGG 2225
QY 1242 CGTGTCAAGTGCGACATCTCGGACCTGCTCCCTCATCTCGCTGTGGTTCGTGGTGGACCC 1301
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QY 2286 TGTGCTCAAGTGTGACATCTCGGACCTGCTCGCTCATCTGCTGTGGCTACAGATGCT 2285
QY 1302 GCTGATGCTACGTGTAAGTGTGATCGGCATCAAGACCGAGCGGTGCCGAGACCTTCAA 1361
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QY 2286 GCTCATGCTCAGTGCACCGTGTATGCCATCAAGACACGCGCGTGGCCGAGACTTCAA 2345
QY 1362 CGAGGCCAAGCCCATCGGCTTCAACATGTAACACCTGCAATTTGTCTGGCTGGCTTCAT 1421
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QY 2346 TGAGGCCAAGCCCATTTGGCTTCAACATGTACACCACTTGCATCGTCTGGCTGGCTTCAT 2405
QY 1422 CCCCATCTTTTGGCACCTCAGTGCAGCGACGAGCTGTACATCCAGACCAACCACT 1481
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QY 2406 CCCCATCTTTTGGCACCTCAGTGCAGCGACGAGCTGTACATCCAGACCAACCACT 2465
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QY 2466 GACGCTCTCCGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGGATGCTCTACATGCCCAAGT 2525
QY 1542 CTACATCATCTCTTCCACCGGAGCAAGCTGCGCCCAAGCGCAAGCGCTCTCAAAGC 1601
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QY 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAAACCTTGAGACCCGAGCGCTGGCTACCAACA 1721
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QY 2646 CGGAGAGCCCAAGTCTGAGCTCTGGAGAACTTTGAGGCCCCAGCGCTGGCCACCAACA 2705
QY 1722 GACCTACCTACCTACCAACCAATGCCATC 1752
Db |||
QY 2706 GACTTACGTCTACTACCAACCAATGCAATC 2736
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RESULT 9
US-09-817-464-1
; Sequence 0, Application US/09817464
; Patent No. 6515107
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Rainer
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,

; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/09/817,464
; CURRENT FILING DATE: 2001-03-26
; EARLIER APPLICATION NUMBER: US/08/617,785
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO SEQ ID NO 1
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2736)
US-09-817-464-1

Query Match 83.6%; Score 1467.8; DB 4; Length 2736;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1559; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
QY 42 AGGTTTCGACCGATCTTCTCCAGCGCACGCTGGACAAACAGAGGCGCAACATCTGGTT 101
Db |||
QY 1026 AGGTTTCGACCGATCTTCTCCAGCGCACGCTGGACAAACAGAGGCGCAACATCTGGTT 1085
Db |||
QY 102 TGGCGAGTTCTGGGAGGACAACTTCCATTCAGTTGAGCGCGCACCGCTCAAGAAGGG 161
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QY 1086 TGGCGAGTTCTGGGAGGACAACTTCCATTCAGTTGAGCGCGCACCGCTCAAGAAGGG 1145
QY 162 AGCCACATCAAGAAGTGCACCAACCGAGAGCGCATCGGCGAGACTCGGCGCTATGAGCA 221
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QY 1146 CAGCCACGTCAAGAAGTGCACCAACCGTGAAGCAATTTGGGCGAGATTCAGCTTATGAGCA 1205
QY 222 GGAGGGGAAGTGCAGTTCTGTGATGAGCTGTGATCGCATGGCGCCACGCGCTGCACGC 281
Db |||
QY 1206 GGAGGGGAAGTGCAGTTCTGTGATGAGCTGTGATCGATGCGGTGATCGCATGGCGCCACGCGCTGCACGC 1265
QY 282 CATGCACCGTGACCTGTGTCCCGCGCGCTAGGACTCTGCCCTCGCATGGAACCCCGTGA 341
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QY 1266 CATGCACCGTGACCTGTGTCCCGCGCGCTAGGACTCTGCCCGCGCATGGACCCCTGTAGA 1325
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QY 1506 AATAGAGCGGATGAGTGGCGGAGGAGCAGCTGCGCGCTCCATCTCGAGCT 1565
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QY 1566 GCCTGCGGAGCGGAGGAGGAGGAGTGTGAAGGAGTGGCTTGTGCTGGCACTG 1625
QY 642 CGAGCCCTGCAACCGGCTACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCTTA 701
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QY 1626 CGAGCCCTGCAACCGGCTACCAAGTGGACCGCTACACCTGTGAAGACCTGCCCTTA 1685
QY 702 CGACATCGGCGCCACAGAGAACCGCAGCAGCTGCGAGCCCATCCCATCTCAAGTTGA 761
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QY 1686 TGACATCGGCGCCACAGAGAACCGCAGCAGCTGCGCGCCCATCCCATCATCAAGCTGA 1745

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Db 1576 AGACTGGATGGAGGCCCTGCAATGGTGTGGGACCCCGACGAGGTGCCCTCGTCTCTG 1635
Qy 574 TGCAGTCTGCCCTGCAGCCCGGGGAGCAAGAAAGACTGTGAAGGGCATGGCTTGCTGC 633
Db 1636 TGCAGCTGCCCTGCAGCCCGGGGAGCGGAAGAGATGGTGAAGGGGTGCCCTGCTGT 1695
Qy 634 TGGCACTGGAGCCCTGCACCGGGTACCAAGTACCAAGTGGACCGCTACACCTGTAAAGACC 693
Db 1696 TGGCACTGGAGCCCTGTGACGGGTACCGGCTTCCAGGTGGACGATTCACATGCGAGGCC 1755
Qy 694 TGCCCTACGACATCGGCCACAGAGAACCGCAGCTGCCAGCCATCCCATCGTC 753
Db 1756 TGTCTGGGGACATGAGGCCACAGCCCAACACAGGGCTGCCGCCACCACTGTGGTG 1815
Qy 754 AAGTTGGAGTGGGACTCGCCGTGGCCGTGTCTTCCCTGGCGGTGGTGGCATC 813
Db 1816 CGCCTGAGTGTCTCCCTGGGCGCCCGCGCTCTCTTGGCGGTGTGGCATC 1875
Qy 814 GCCGCCACGCTGTTCTGGTGTGACGTTGTGGCTACAGATACACCCCATCGTCAAG 873
Db 1876 GTGGCCACTACCAACGTTGTGGCCACCTTCTGTGGGTACAAACACGCCCATCGTCCGG 1935
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Db 1936 GCCTCGGGCCGAGACTCAGCTACGCTCTCTTCCACCGGCATCTTCTCATACGCCATC 1995
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Db 1996 ACCTTCTCATGCTGCTGAGCCTGGGCGCGGTCTGTGCGCGCGAGGCTCTTCTCTG 2055
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Db 2056 GGGCTGGGCGACGACCTCAGCTACTCTGCCCTGTCTCACAAGACCAACCGTATCTACCGC 2115
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Db 2236 GCCCGGCCCCACACAGCGGTATTGACTATGAGGAAACAGCGGACGGTGGACCCCGAGCAG 2295
Qy 1234 GCCAGGGGCTCAAGTGGACATCTCGACCTGCTCCCTCATCTGCTGCTGGGTAC 1293
Db 2296 GCCAGAGGGTCTCAAGTGGACATCTCGGATCTGCTCTCATCGGCTGGGTGGGTAC 2355
Qy 1294 AGCATGCTGCTGATGGTCAAGTGTACTGTGACGCGCATCAAGACCCGAGGGGTGCCGAG 1353
Db 2356 AGCCTCTGCTCATGCTCAGGTGACAGTGTAGCGCCATCAAGGCCCGGTGGCGTGGCCGAG 2415
Qy 1354 ACCTTCAACGAGGCCAAGCCCATCGGCTTACCATGATACACCATGCTGCTGGGTG 1413
Db 2416 ACCTTCAACGAGGCCAAGCCCATCGGCTTACCATGATACACCATGCTGCTGGGTG 2475
Qy 1414 GCCTTCATCCCATCTTTTGGCACTTCAGTCCAGCGGACAGCTGTATCATCAGACA 1473
Db 2476 GCATTCGTGGCCATCTTTTGGCACTGCCAGTCCAGTGAAGAGATCTATCATCAGACA 2535
Qy 1474 ACCACACTGACGGTCTCGGTGAGTCTGAGCGCTTCAGTGTCCCTGGGATGCTCTACATG 1533

Db 2536 ACCACGCTAAACCGGTCTTTGAGCCTGAGTGCCTCGGTGCTCCCTCGGCATGCTCTACGTA 2595
Qy 1534 CCCAAGCTTACATCATCTCTTCCACCGGAGCAGACGTCGCCCAAGCGCAACGCGAGT 1593
Db 2596 CCCAAAACCTACGTCATCTCTTCCATCCAGAGCAGAAATGTGCAGAAAGCGGAGC 2655
Qy 1594 CTCAAACCGGTGGTCCACCGCGCCACCATGTCCTCAA 1628
Db 2656 CTCAAGGCCACCTCCACGCGTGGCAGCCGCCACCAA 2690

RESULT 11
US-09-277-858-1
; Sequence 1, Application US/09277858
; Patent No. 6362316
; GENERAL INFORMATION:
; APPLICANT: Dagget, Lorrie
; Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; SUBTYPE mGluR6, NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/277,858
; FILING DATE: 26-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,875
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9921
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2961 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 85..2718
; OTHER INFORMATION: /product= "Human Metabotropic
; Glutamate Receptor Subtype mGluR6"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-277-858-1

Query Match 50.2%; Score 880.6; DB 3; Length 2961;
Best Local Similarity 72.5%; Pred. No. 1.1e-192;
Matches 1156; Conservative 0; Mismatches 430; Indels 9; Gaps 1;
Qy 43 GGGTTCCAGCATCTTCTCAGCGCCGACGCTGCAGCAACACAGCGCGCAACATCTGGTTT 102
Db 1096 GGATTTGACGAGTACTTCTGATCTCGATCTCTGGAGAACCAACCGCAGGACATCTGGTTC 1155
Qy 103 GCCGAGTCTCTGGGAGGACAACTTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAGGGA 162

Db 1156 GCGAGTTCCTGGGAAGAGAAATTTAACTGCAAACTGACCACTCAGGTACCCAGTCAGAT 1215
Qy 163 AGCCATCATAGAAAGTGCACCAACGAGAGCGCATCGGGGACGAGACTCGGCCTATGAGCAG 222
Db 1216 GATTCCACCGCAATGCAACGCGGAGAAACGATCGGCGGGACTTCACACTACGAGCAG 1275
Qy 223 GAGGGGAAGGTGAGTTCGTGATTGACGCTGTGTACGCCATGGCCACCGGCTGACGCC 282
Db 1276 GAGGGCAAGGTGAGTTCGTGATTGATGCGGTGTATGCCATTGCCACGCCCTCCACAGC 1335
Qy 283 ATGCACCGTGACCTGTGTCGCCGCCGCTAGGACTCTGCCCTCGCATGACGCCCGGTGAT 342
Db 1336 ATGCACCGCGCTCTGCCCTGGGCACACAGGCTGTGCCCGGATGGAACCCACCGAT 1395
Qy 343 GGCACCGAGTGTAAAGTACATCAGAAAGCTCAACTTCTCAGGCATTCGGGGAAACCT 402
Db 1396 GGGCGGATGCTTCGAGTACATCCAGCTGTCCGCTTCAACGGCAGCGCAGAAACCCCT 1455
Qy 403 GTAACTTCAATGAGAACGAGACGACCGGGGCGCTACGATCTACAGTACCACTG 462
Db 1456 GTGATGTTCAACGAGAACGGGATGCGCCCGGGCGGTACGATCTTCCAGTACCAAGCG 1515
Qy 463 CGCAATGGCTCGGC-----CGAGTACAAAGTTCATCGGCTCGTGGACAGACCACTG 513
Db 1516 ACCAATGGCAGTGCCAGCAGTGGCGGTACAGGCGAGTGGCCAGTGGGACAGACCTC 1575
Qy 514 CACTCAGAAATAGCGGATGAGTGGCCAGGAGTGGCCAGCAGTGGCCGCTCCATC 573
Db 1576 AGACTGGATGTGAGGCGCTCGAGTGTCTGGGACCCCAAGAGTGGCCCTCGTCTG 1635
Qy 574 TCGAGTTCGCTGCGAGCGCGGGAGCGAAGAGACTGTGAAGGCATGCTTGTGCG 633
Db 1636 TGACGCTCCCTGCGGCGGGGAGCGAAGAGTGGTGAAGGCGCTCCCTGCTGT 1695
Qy 634 TGGCACTGCGAGCGCTGCAACCGGTACCAAGTGGACCGCTACACCTGTAAAGC 693
Db 1696 TGGCACTGCGAGCGCTGTACCGGTACCGCTTCAGGTGGACGATTCACATGCGAGGC 1755
Qy 694 TGCCCTACGACATGCGGCGCCACAGAAACCGCAGAGTGGCCAGCCATCCCACTGTC 753
Db 1756 TGTCTGGGACATGAGGCGCCACGCCAACACACAGCGGCTGCGGCCCAACACTGTG 1815
Qy 754 AGTTGGAGTGGACTCGCGGTGGCGGTGCTGCGGCTCTTCTGCGCGTGTGGGCATC 813
Db 1816 CGCTGAGTGTGCTCCCTGCGGCGCGCGCTCTCTGCGCGTGTGGGCATC 1875
Qy 814 GCGCGCACGCTGTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873
Db 1876 GTGGCACTACACGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1935
Qy 874 GCTCGGCGCGGAACTGAGCTACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 933
Db 1936 GCTCGGCGCGGAGCTACGTACGTCTCTCTCACCGCATCTTCTCATCTACGCCATC 1995
Qy 934 ACCTTCTCATGATGCGAGCGGACCTGCGGAGACTGTTGCTGCTGCGCGCATCTTCTTA 993
Db 1996 ACCTTCTCATGATGCTGAGCTGCGGCGCGGCTGTGCGCGCGCGGCTCTTCTG 2055
Qy 994 GGGCTCGGATGAGCATGAGCTACGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1053
Db 2056 GGCCTGGGACGACCTCAGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2115
Qy 1054 ATCTTTGAGCAGGCAAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1113
Db 2116 ATCTTTGAGCAGGCAAGCGCTCGGTACACACCCCTCTCTTCTCATGCGCCACCTCAC 2175
Qy 1114 CTGGCGATCACCCTTATCTCTATCTCTCTGAGCTGCTGCGCATCTGCGTGTGTTG 1173
Db 2176 CTGGTATCACCCTTACCTCTCTCTGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2235
Qy 1174 GTGGACCCCTCCACTCGGTGGTGGATCTCCAGGACCAACGACACTTGAACCCCGCTT 1233
Db 2236 GCGCGGCGCCCAACAGCGGTGATTGACTATGAGGAACAGCGGACCGGTGACCCCGAGCAG 2295

Qy 1234 GCCAGGGGGTGTCTCAAGTGGAGCATCTCGGACCTGTCTCTCATCTGCTGTGGCTTAC 1293
Db 2296 GCCAGAGGGGTGTCTCAAGTGGAGCATCTCGGATCTGTCTCTCATCGGCTGCTGTGGCTTAC 2355
Qy 1294 AGCATGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1353
Db 2356 AGCTTCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2415
Qy 1354 ACCTTCAACGAGGCCAAGCCCATCGGCTTACCATGTATACCACTGTGATCTGTGGCTG 1413
Db 2416 ACCTTCAACGAGGCCAAGCCCATCGGCTTACCATGTATACCACTGTGATCTGTGGCTG 2475
Qy 1414 GCCTTATCCCATCTCTTTTGGCACTCTACAGTACGCGCAAGCTGTATCTCAGACA 1473
Db 2476 GCATTCGTGCCCATCTCTTTTGGCACTCTCAGTACGCTGAAAGATCTTACATCCAGACA 2535
Qy 1474 ACCACATGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1533
Db 2536 ACCACGCTAACCGTGTCTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2595
Qy 1534 CCCAAGTCTACATCTCTTCCACCGGAGCAGAAAGCTGCGCCCAAGCGCAAGCGCAGT 1593
Db 2596 CCCAAGTCTACATCTCTTCCACCGGAGCAGAAAGCTGCGCCCAAGCGCAAGCGCAGT 2655
Qy 1594 CTCAAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1628
Db 2656 CTCAAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2690

RESULT 12

US-09-126-280-1

; Sequence 1, Application US/09126280

; Patent No. 6103524

; GENERAL INFORMATION:

; APPLICANT: Wu, Su

; APPLICANT: Belagaje, Rama M

; TITLE OF INVENTION: Metabotropic Glutamate Receptor Protein and Nucleic

; FILE OF INVENTION: Acid

; FILE REFERENCE: Sequence List

; Patent No. 6103524

; CURRENT APPLICATION NUMBER: US/09/126,280

; CURRENT FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 2670

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (13)..(2643)

US-09-126-280-1

Query Match 49.6%; Score 871; DB 3; Length 2670;

Best Local Similarity 72.1%; Pred. No. 1.7e-190;

Matches 1150; Conservative 0; Mismatches 436; Indels 9; Gaps 1;

Qy 43 GGGTTCGACCGATCTTCTCCAGCGGACGCTGGACCAACAGCGCAACATCTGTTT 102
Db 1024 GGAATTTGACCGATCTTCTCCAGCGGACGCTGGACCAACAGCGCAACATCTGTTT 1083
Qy 103 GCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCCGCCAGCTCAAGAGGGA 162
Db 1084 GCCGAGTTCTGGGAGGAGAAATTTAACTGCAAACTGACCACTCAGTACCGTACAGT 1143
Qy 163 AGCCATCAAGAGTGCACCAACGAGAGCGCATCGGGAGGACTCGGCTATGAGCAG 222
Db 1144 GATTCCACCCCAAAATGACAGGCGAGAAAGCATCGGCGGGAATCCACCTACGAGCAG 1203
Qy 223 GAGGGAGGTGAGTTCGTGATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 282
Db 1204 GAGGGAGGTGAGTTCGTGATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263

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Oy 283 ATGCAACCGTGACCTGTGTCCGGCCGCGTAGGACTCTGCTCGCATGAGACCCCGTGGAT 342
Db 1264 ATGCAACGAGCGCTCTGCGCTTGGGACACAGGCGCTGTGCCGGGATGGAACCCACCGAT 1323
Oy 343 GGCACCCAGCTGCTTAAGTACATCAGGAACGTCACCTTCTCAGGCATTTGCGGGAAACCT 402
Db 1324 GGGCGGATGCTTCTGCACTACATTGAGCTGTGCGCTTCAATGGCAGCGCAGGAACCCCT 1383
Oy 403 GTAACCTTCAATGAGAACGGAGACGCCACGGGGCGCTAGGACATCTACAGTACCAACTG 462
Db 1384 GTGATGTTTCAAGAGAACGGGATGCGCCCGGGCGGTACGACATCTTCCAGTACCAAGCG 1443
Oy 463 CGCAATGCTCGGC-----CGAGTACAAGGTTCATCGCTCGTGACAGACCACTG 513
Db 1444 ACCAATGCACTGCCAGAGTGGCGGGTACAGGCACTGGGCGGAGTGGGCGAGACCCCTC 1503
Oy 514 CACCTCAGAAATAGAGCGGATGAGTGGCCAGGAGTGGCCAGCAGCTGCCCGCTCCATC 573
Db 1504 AGACTGGATGTGGAGGCCCTGCAGTGTGTGCGACCCCAACGAGGTGCCCTCGTCTCTG 1563
Oy 574 TGCAGTGTCCCTGCACGCCCGGGAGCGAAAGAACTGTGAAGGCAATGGCTTGCTGC 633
Db 1564 TGCAGCTGTCCCTGCAGGCGCGGGAGCGGAAGAGATGGTGAAGGGCGTCCCTCGTGT 1623
Oy 634 TGGCACTCGAGCCCTGCACCGGGTACCAGTACCAGTGGACCGCTACACCTGTAAAGAC 693
Db 1624 TGGCACTCGAGGCGCTGTGACGGGTACCGCTTCCAGGTGGAGGATTTACATGCGAGGCC 1683
Oy 694 TGCCCTCAGCAGATCGGCCCCACAGAGAACCGCAGCTGCCAGCCCATCCCATCGTC 753
Db 1684 TGTCTGGGGACATGAGGCCCAACGCGCCCAACACAGCGGCTGCGGCCCCACACCTGTGTG 1743
Oy 754 AAGTGGAGTGGAACTCGCGGTGGCGGTGTGCGCCCTTCTTGGCGCGTGGTGGGCATC 813
Db 1744 CGCTGAGCTGTCTCCCTCGGGCAGCGCGCGCTCTCTGCGCGCTGTGGGCATC 1803
Oy 814 GCGCCACGCTGTTCGTGTGTGTACGTTGTGGCTACAAGTACACCCCATCGTCAAG 873
Db 1804 GTGGCCACTACCAACGGTGTGGCCACCTTGTGGCGGTAAACAACAGCCCATGTTCGG 1863
Oy 874 GCCTCGGCGCGGAACTGAGCTACGTGTGTGTGGCGGCGATCTTTCTGTGTAGCCACT 933
Db 1864 GCCTCGGCGCGGAACTCACTAGCTCTCTCTCACCGCATCTTCTCTATCTACGCCATC 1923
Oy 934 ACCTTCTCTATGATCGCAAGCGGACCTGTGGGACCTGTGCTCGCGCGCATCTTCTTA 993
Db 1924 ACCTTCTCTATGCTGAGCTGTGGGCGCGGCTGTGTGCGCGCGCAGGCTCTTCTCTG 1983
Oy 994 GGGCTCGGCATGAGCATCAGCTACGCGGCGCTGTGACCAAGACCAACCGCATTTACCGC 1053
Db 1984 GGCCTGGGCGAGACCTCAGCTACTCTGCCCTGTCTACCAAGACCAACCGTATCTACCGC 2043
Oy 1054 ATCTTTGAGCAGGGCAACCGTCTGCTGAGTGCCTCGCTTTTCATCAGCCCGGCTCGCAG 1113
Db 2044 ATCTTTGAGCAGGGCAAGCGTCTGCTACACCCCTCTCTTTCATCAGCCCGGCTCGCAG 2103
Oy 1114 CTGGCCATCATTCACTCATCTATCTCTGAGCTGTCTGCGCATCTGCGTGTGGTTCGTG 1173
Db 2104 CTGTGTATCACCCTCAGCTCTACCTCTCTGAGTGTGTGGGATTAATACATGGTGGGG 2163
Oy 1174 GTGGACCCCTCCCACTCGGTGTGTGACTTCAGGACCAACGACATTTGACCCCGCTTT 1233
Db 2164 GCGCGGCCCCACACAGCGTGTATGACTATAGGAAACAGCGGACGGTGGACCCCGAGCAG 2223
Oy 1234 GCGAGGGGTGCTCAAGTGGACATCTCGGACCTGTCTCTCATCTGCTCTGTGGGTAC 1293
Db 2224 GCGAGGGGTGCTCAAGTGGACATCTCGGATCTGTCTCTCATCTGCTGTGGGTAC 2283
Oy 1294 AGCATGCTGTGATGGTCACTGTGTATCGCCATCAAGACCGGAGGGTGGCCGAG 1353
Db 2284 AGCTCTCTGTCTATGTCAGCTGCACTGTATCGCCATCAAGGGCCGTGGGTGGCCGAG 2343
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Oy 1354 ACCTTCAACGAGCGCAAGCCCATGGGCTTCCATGTACACCACTGCATGTCTGGCTG 1413
Db 2344 ACCTTCAACGAGCGCAAGCCCATGGGCTTCCATGTACACCACTGCATGTCTGGCTG 2403
Oy 1414 GCCTTATCCCATCTTTTGGCACTTCAAGTCAAGCCGACAGCTGTATCATCCAGACA 1473
Db 2404 GCATTCGTGGCCATCTTTTGGCACTGCCAGCTCAGCTGAAAGATTTTATCATCCAGACA 2463
Oy 1474 ACCACACTGACGGTCTCCGTGAGTCTGAGCGCTTTCAGTGTCCCTGGGGATGCTCTACATG 1533
Db 2464 ACCACGCTAACGGTCTTTCAGCTGAGTGCCTCGGTGTCCCTCGGCATGTTTATGCTA 2523
Oy 1534 CCCAAGTCTTACATCATCTCTTCCACCCGAGCAGAACGTCGCCAAGCGCAACGCGCAGT 1593
Db 2524 CCCAAAACCTAGCTCATCTTTTCCATCCAGAGCAGAAATGTGCAAGAGCGAAGCGGAGC 2583
Oy 1594 CTCAAGCCGTGTGCACCGCGCCACCATGTCCNA 1628
Db 2584 CTCAAGGCCACCTCCACGCTGGCAGCCGCCCCCA 2618

RESULT 13
US-09-126-280-3
; Sequence 3, Application US/09126280
; Patent No. 6103524
; GENERAL INFORMATION:
; APPLICANT: Wu, Su
; APPLICANT: Belagaje, Rama M
; TITLE OF INVENTION: Metabotropic Glutamate Receptor Protein and Nucleic
; FILE OF INVENTION: Acid
; FILE REFERENCE: Sequence list
; Patent No. 6103524
; CURRENT APPLICATION NUMBER: US/09/126,280
; CURRENT FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2635
; TYPE: RNA
; ORGANISM: Human
US-09-126-280-3

Query Match 49.0%; Score 860.2; DB 3; Length 2635;
Best Local Similarity 57.7%; Pred. No. 5.2e-188;
Matches 945; Conservative 229; Mismatches 448; Indels 15; Gaps 3;

Oy 7 GGGGTATCATCATCTTTTGGCCAAAGAGATGATC--AGGTTGACGGTACTTCTCCA 64
Db 974 GGGCAUCACCAUCUCGCCCAAAAGGGCCUCCAUCCGACGGAUUGACGACUACUACA 1033
Oy 65 GCGCACGCTGGACAAACACAGCGCAACATCTGTTTGGCGAGTCTTGGGAGGACAACT 124
Db 1034 CUCGAUCCCGGAGAGAACACCGAGGAACAUCUGGUGCCGAGUUCUGGAGAGAGAAU 1093
Oy 125 TCCATTGCAAGTTGTAGCGCGCCACCGCTCAAGAGGGAAGCCACATCAAGAAGTGCAC-- 182
Db 1094 UUAACUGCAACUGACGACGACUCCAGUACCCAGUACAGAUUCCACCGCAAAUGCAG 1153
Oy 183 --CAACGAGAGCGCATCGGGCAGGACTCGGCTTATAGCAGGAGGAGGAGGAGTTC 240
Db 1154 GUCUACGAGGAACACUCCGCGCGGACUCCACUACGAGCAGGAGGAGGAGGAGU 1213
Oy 241 GTGATTACGCTGTGTAGCCATGGGCGCAGCGCTGCACGCGCATGACCGGTGACTGTGT 300
Db 1214 GUGAUAUGCGGUGAUGACCAUUGCCCAAGCCUCCACAGCAUGACACGAGCGCUCG 1273
Oy 301 CCGCGCGCGTGTAGGACTCTGCTTGCATGAGACCCCGTGGATGGCAACCCAGCTCTTAAG 360
Db 1274 CCUGGGCACACAGCGCUGUGCCCGCGAUGAAACCCACCGAGGCGGAGUUCUUCUGCAG 1333
Oy 361 TACATAGGAACGTCATCTTCTAGGCACTTTCAGGCACTTTCGGGGGAACTCTTAACCTTCAATGAGAAC 420
Db 1334 UACAUCGAGCUGUCCGCUCAUUGGCGAGGAGACCCCGUGUGAUGAUCACGAGAAC 1393
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QY 421 GGAGAGCGACCGGGGCGCTACGACATCTACAGTACCACTACGCGCAATGCGCTCGGC----- 476
DB 1394 GGGGAUGCGCCCGGGCGGACGACCAUUCUCCAGUACACAGCGACCAUUGGCGAGUGCCAGC 1453
QY 477 -----CGAGTACAAGGTCACTCGCTCGTGACAGACCACTGCACCTCAGATAGAGCGG 531
DB 1454 AGUGGCGGUAACAGGACAGUGGGCCAGUGGGAGAGACCCUACAGACUGGAUGGAGGCC 1513
QY 532 ATGCACTGCGGAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCACTGCGCTGCGCTGCGCAG 591
DB 1514 CUGCAGUGGUCUGGCGACCCCAAGGUGCCUUCUGUCAGGCGCCUUCUGUCAGCCUUCGCGG 1573
QY 592 CCGGGGAGCGAAGAGACTGTGAAGGCGATGGCTTGTCTGCTGCGACTGCGAGCCCTGC 651
DB 1574 CCGGGGAGCGAAGAGGUGGAGGCGGCGCCUUCUGUCUGGCGAGCGGCGGCGU 1633
QY 652 ACCGGGTACAGTACCAAGTGACCGCTACACTGTGAAGACTGCCCTTACGACATGCGG 711
DB 1634 GAGGGUACCGUUCAGGUGGAGCAGUUCACAUUGGAGGCGUUCUGGCGGAGAGG 1693
QY 712 CCCAGAGAACCGCAGAGCTGCCAGCGCCATCCCATCGTCAAGTTGGAGTGGAGCTCG 771
DB 1694 CCCAGCCCAACACAGCGGCGCGGCCCCACACUGUGGCGGCGGAGUGGCGUCC 1753
QY 772 CCGTGGCGCTGCTGCTCTTCTGCGGTGGTGGCATCGCGCGCAGCGCTGTGCTG 831
DB 1754 CCGUGGCGACCGCGCGCUCUCUGCGCGGUGGCGUUGGCGGCAUCCAGCGGUG 1813
QY 832 GTGGTCACTGTTGCGGTACAGCATACCCCATCGTCAAGCGCTCGGCGCGGAGCTG 891
DB 1814 GUGGCGACCCUUGUGGCGUACACACACCGCCCAUGCGCGGCGUCCGGCGGAAACUC 1873
QY 892 AGCTAGCTGCTGCTGCGGGCATCTTCTGTGCTAGCGCCACTACTCTTCATGATCGCA 951
DB 1874 AUAUAGUUCUUCACCGGCAUUCUUCUACUAGCGCAUCCUUCUUGGUGGCU 1933
QY 952 GAGCGGACCTGGGACCTGTTGCTCGCGCATCTTCTAGGCGTGGCATGAGCATC 1011
DB 1934 GAGCGGCGCGCGGUGUGCGCGCGCAGCGCUCUUCUGGCGCGGCGACCGCCUC 1993
QY 1012 AGCTAGCGCGCTCTGACCAAGACCAACCGCATTTACCGCATCTTTGAGCAGGCGAA 1071
DB 1994 AGCUACUGCGCGUUCUACCAAGACCAACCGCAUCCGCAUCCGCAUUGGAGGCGAAG 2053
QY 1072 CCGTGGTCACTGCGCGGCTTCTATCAGCGCGGCTCGCAGCTGGCCATCACTTTCATC 1131
DB 2054 CGCGGUAACACCCUUCUACUAGCGCCCAUCCUACAGCUGGUGUACUACCUUACG 2113
QY 1132 TCTATCTCCCTGAGTGTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191
DB 2114 CUCACUCCUGCAGGUGGUGGGAUUAUACUUGGUGGCGCGCGCGCGCCACACAGC 2173
QY 1192 GTGGTGGACTCCAGGACCAAGGACATTTGACCCCGCTTTCAGGCGGCTGCTGCTGCTG 1251
DB 2174 GUGAUGGUAUGAGGACAGCGGACGUGGCGCGCGGAGCGGCGGCGGUGGUGGUGG 2233
QY 1252 TCGGACATCTCGGACTGCTGCTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
DB 2234 UGCGACUUGGUAUUGUUCUACUAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2293
QY 1312 ACGTGTACTGTGTACGCCATCAAGACCCGAGCGGTGCGCGAGACTTTCAGAGGCGCAAG 1371
DB 2294 ACGUGCAGAGUGUACGCCAUAAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2353
QY 1372 CCCATGCGCTTACCATGTAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1431
DB 2354 CCCAUGGCGUACCAUGUACACCAUCCUGCAUCCUGGCGGCGGCGGCGGCGGCGG 2413
QY 1432 TTTGGCACCTCAGTTCAGCGACAGCTGTATCTCAGACACACACACTGACGCTGCTCC 1491
DB 2414 UUGGCAUUGCGGCGUAGGUAAGAUUAUACUCCAGACCAACCGUACCGGUGUCC 2473

QY 1492 GTGAGTCTGAGCGCTTCACTGTCTGCGGATGCTCTATATGCCCAAGTCTTACATCATC 1551
DB 2474 UUGAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2533
QY 1552 CTCCTTCCACCGCGGAGCAGAACTGCGCCAGCGCAGGCTCTCAAAGCGCTGGTCAAC 1611
DB 2534 UUUUCCCAUCCAGCAGAGAGUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2593
QY 1612 GCCGCCACCATGTCCAA 1628
DB 2594 GUGGAGCGCCACCCAA 2610

RESULT 14

US-08-855-146-1
; Sequence 1, Application US/08855146
; Patent No. 6221609
; GENERAL INFORMATION:
; APPLICANT: Belagaje, Rama M.
; APPLICANT: Wu, Su
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Department
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855.146
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,243
; FILING DATE: 07-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-6334
; TELEFAX: (317) 276-2764
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..2781
US-08-855-146-1

Query Match 47.8%; Score 839; DB 3; Length 3321;
Best Local Similarity 68.6%; Pred. NO. 4.1e-183;
Matches 1173; Conservative 0; Mismatches 535; Indels 3; Gaps 1;

QY 43 GGGTTCGACCATCTTCTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 102
DB 1075 GGATTTGATCGATCTTTAGAAAGCGGAACTCTTGCAATATATCGAAGAAATGTGTGGTTT 1134
QY 103 GCCGAGTTCTGGGAGGACAACTTCATTGCAAGTTGAGCGCGCGCGCTCAAGAAGGA 162
DB 1135 CGAATTTCTGGAGGAGAAATTTGGCTGCAAGTTAGATCATTGGG---AAAAGGAAC 1191

SEQUENCE CHARACTERISTICS:
LENGTH: 3321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
US-08-855-146-3

Query Match 47.8%; Score 839; DB 3; Length 3321;

Best Local Similarity 52.5%; Pred. No. 4.1e-183;

Matches 898; Conservative 275; Mismatches 535; Indels 3; Gaps 1;

QY	43	GGGTTGACCGATCTTCTCCAGCGCAGCGCTGGACAAACAGAGCGGCAACATCTGGTTT	102
DB	1075	GGAUUGAUGCAUACUUAAGAACCGCGAAACUCUUGCCAAUUAUCGAGAAUUGUGUGUUU	1134
QY	103	CGCGAGTCTCGGAGGACAACTTCCATTGCAAGTTGAGCCGCGCAGCGCTCAAGAGGGA	162
DB	1135	GCAGAAUUCUGGAGGAGAAUUUUGGUGCAAGUUAAGGAUCAUGGG---AAAGGAAC	1191
QY	163	AGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCGCTATGAGCAG	222
DB	1192	AGUCAUAUAAAGAACGACAGCGGCGAGCGAAUUGCUGGGAUUAUCAUUAUGAACAG	1251
QY	223	GAGGGAAGTGCAGTTCTGATTGACGCTGTGTAGCGCATGGGCCACGCGCTGCACGCC	282
DB	1252	GAAGAAAGGUCCAAUUUUAUUAUGAUGUGUAUUAUCCAUUGGCUUACGCCUCGACAAU	1311
QY	283	ATGACCGTGTACTGTGTCGCGCGCGTGGAGCTCTGCCCTCGATGGACCCCGTGGAT	342
DB	1312	AUGCAAGAAGUUCUGCGCCGGAUACAUGGCGCUUUGCCAGAAUGAGUAACCAUUGAU	1371
QY	343	GGCACCCAGCTCTTAAAGTACATCAGGAACGTCACCTTCTCAGGCAATGCGGGAACCTT	402
DB	1372	GGGAAGAGCUACUUGUUAUUAUUGGCGUGUAUUAUUAUGGCGUGGCGACUCUU	1431
QY	403	GTAACTTCAATAGAAACGAGACGCAACGCGGCGGTACGACATCTACAGTACCAATG	462
DB	1432	GUCAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1491
QY	463	CGCAATGCTCGGCGGAGTACAGCTCATCGCTCGTGAGACACCACTGACCTCAGA	522
DB	1492	ACCAACAAAGCACAGAGUACAAGGUCACGCGCCACUGGACCAUACGCUUACUCAA	1551
QY	523	ATAGAGCGGATGACGTGGCCGAGTGGCCAGAGCTGCCCGCTCCATCTGCACTGTG	582
DB	1552	GUGGAAGACUAGCAGUGGCUCAUAGAGNACAUAUCACCCGCGUUGUUGGCGGCU	1611
QY	583	CCCTGCCAGCCCGGAGCGAAGAGACTGTGAAGGGGCAAGGCTTGTGCTGGCACTGC	642
DB	1612	CGUGUAGCCAGGCGAGAGGAAGAAACCGUGAAGAGGGGUGCCUUGUGUGGACU	1671
QY	643	GAGCCCTGCACCGGTACAGTACCAAGTGGACCGCTACCTGTAAAGCTGCCCTTAC	702
DB	1672	GAACCGUGAGAGGUUAACAACACAGGUGGAGUAGCUGUUGGAAUUAUUGGCGCUG	1731
QY	703	GACATGCGGCGCACAGAGAACCGCACAGCTGCCAGCGCCATCCCATCGTCAAGTTGG	762
DB	1732	GAUCAGAGACCCACAUAGAACCGCACAGGCGUCCAGCUUUAUCCCAUACAUAUUG	1791
QY	763	TGGGACTCGCGTGGCGCGTGTGCTCTTCTTCTGGCGTGGTGGGATCGCGCCACG	822
DB	1792	UGGCAUUCUCCUGGCGUGGUGCUUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAU	1851
QY	823	CTGTTCTGGTGGTACGTTTGTGGCTTACAGATACCCCATCGTCAAGSCCTCGGCG	882
DB	1852	ACCUUGUGAUGGAGACCUUUGUCCGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	1911
QY	883	CGGGAACAGTACGTGCTGCGGCGCATCTTCTTCTGTGTACGCCACTACCTTCTCTC	942
DB	1912	CCGGAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	1971
QY	943	ATGATCGCAGAGCCGACCTGGGAGACCTGTTCTGCTCCGCGCATCTTCTTAGGGCTCG	1002

DB	1972	AUGAUGCAGCACCCAGAUACAUAUAGCUCUCCGACGGGUCUUCUUCAGGACUUGGC	2031
QY	1003	ATGAGCATCAGTACGCGGCGCTGTGACCAAGACCAACCGCATTTACCGCATCTTTGAG	1062
DB	2032	AUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2091
QY	1063	CAGGCAAAACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	1122
DB	2092	CAGGGAAGAAUUAUUGUACAGAGCGCCCAAGUUAUUAUUAUUAUUAUUAUUAUUAU	2151
QY	1123	ACCTTATCTCTCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1182
DB	2152	ACCUACGCGCAUUCUGGCGGCUUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2211
QY	1183	TCCCATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	1242
DB	2212	CCCAACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2271
QY	1243	GTGCTCAAGTGCAGATCTCGGACCTGTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTG	1302
DB	2272	GUGCUAAGUGUGACAUUUCUCACUCACUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2331
QY	1303	CTGATGTCAGTGTACTGTGTACGCCATCAAGACCCGAGCGGCTGCCGAGACCTTCAAC	1362
DB	2332	UUGAUGGUCACUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2391
QY	1363	GAGGCAAGCCATCTCGGCTTCCACATGTACACCATCTGCTGCTGCTGCTGCTGCTGCTG	1422
DB	2392	GAAGCAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2451
QY	1423	CCCATCTTTTGGCACCTCAAGTCAGTCAGCCGACCAAGCTGTATCATCCAGACCAACAC	1482
DB	2452	CCCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2511
QY	1483	ACGCTCTCCGTGAGTCTGAGCGCTTCACTGCTCCCTGGGGATGCTTATATGCCCCAAGTC	1542
DB	2512	ACUGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2571
QY	1543	TACATCATCTCTTCCACCCGAGCAGAAACGTGCCCAAGCGCAGCGCATCTTCAAAGCC	1602
DB	2572	UAUAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2631
QY	1603	GTGTCACCGCGCCGACCATGTCCAAAGTTTCAACAGAGGGGCAACTTCAGGCCCAAT	1662
DB	2632	GUGGUGACAGCUGCCACCAUGCAAAAGCAACUGAUCCAAAGGAAUUAUGACAGACCAAU	2691
QY	1663	GGGGAAGCCAAATCAGAGCTGTGTAGAACCTGGAGACCCCGCGCTGGCTACCAACAG	1722
DB	2692	GGCAGGUGAAGGAGAAACUCUGGAGAGUCUUGAAGCAACACUUCUUAUUAUUAUUAU	2751
QY	1723	ACCTAGCTCACCTACACCAACCATGCTCATCT	1753
DB	2752	ACUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	2782

Search completed: June 21, 2005, 08:56:07

Job time : 319 secs

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Result No.	Query			ID	Description
	Score	Match	Length		
1	1755	100.0	1755	ACC70676	Acc70676 Rat gluta
2	1707.6	97.3	2838	ABX16077	Abx16077 Rat cDNA
3	1473.8	84.0	2694	ADO29096	ADO29096 Mouse nov
4	1470.8	83.8	2739	ADO29776	ADO29776 Human nov
5	1470.8	83.8	3431	AAD38025	Aad38025 Human met
6	1470.8	83.8	3431	AAD38024	Aad38024 Human met
7	1470.8	83.8	3884	ABX16087	Abx16087 Human met
8	1470.8	83.8	3884	ABZ42692	Abz42692 Human met
9	1470.8	83.8	3884	ADE07285	Ade07285 Novel cod
10	1470.8	83.8	3884	ACA56476	Aca56476 Human sig
11	1470.8	83.8	3884	ADI56272	Adi56272 Human pol
12	1470.8	83.8	3884	ADQ89113	Adq89113 Human uro
13	1469.2	83.7	3880	ATQ3888	Atq3888 Human mgl
14	1468.2	83.7	2738	AAQ89342	Aaq89342 Human mgl
15	1422.8	81.1	3470	ADRO6667	Adr-06667 Full leng
16	1340.6	76.4	3590	ADR10413	Adr10413 Full leng
17	1337.8	76.2	4271	ACN43319	Acn43319 Human dia
18	1311.2	74.7	4342	ACN43318	Acn43318 Human dia
19	880.6	50.2	2634	ADO29778	Ado29778 Human nov
20	880.6	50.2	2961	ANT38322	Ant38322 Metabotro

Db 1490 GCTGATGTCAGTGTACTGTGTACGCGCATCAAGACCCGAGGCGTGTCCGAGACCTTCAA 1549
Qy 1362 CGAGGCCAAGCCATCGGCTTCAACATGTACACCACTGCAATGTCTGGCTGGCTTCAT 1421
Db 1550 CGAGGCCAAGCCATCGGCTTCAACATGTACACCACTGCAATGTCTGGCTGGCTTCAT 1609
Qy 1422 CCCCATCTTTTGGCACTCACAGTCAAGCGAGCAAGCTGTACATCCAGACACCACT 1481
Db 1610 CCCCATCTTTTGGCACTCACAGTCAAGCGAGCAAGCTGTACATCCAGACACCACT 1669
Qy 1482 GACGCTCTCCGTAGTCTGAGCGCTTCAAGTGTCCCTGGGGATGCTCTACATGCCCAAGT 1541
Db 1670 GACTGTCTCCGTAGTCTGAGCGCTTCAAGTGTCCCTGGGGATGCTCTACATGCCCAAGT 1729
Qy 1542 CTACATCATCTCTTCCACCGGAGCAGAAAGTGTCCCAAGCGAGCGAGCTCTCAAGC 1601
Db 1730 CTACATCATCTCTTCCACCGGAGCAGAAAGTGTCCCAAGCGAGCGAGCTCTCAAGC 1789
Qy 1602 CGTGTACACCGCGCCACCATGTCCAAAGTTTCAACAGAGGCGCACTTCAGGCCAA 1661
Db 1790 CGTGTACACCGCGCCACCATGTCCAAAGTTTCAACAGAGGCGCACTTCAGGCCAA 1849
Qy 1662 TGGGAAGCCAAATCAGAGCTGTGTGAGAACCTGGAGACCCGCGCTGGCTACCAACA 1721
Db 1850 TGGGAAGCCAAATCAGAGCTGTGTGAGAACCTGGAGACCCGCGCTGGCTACCAACA 1909
Qy 1722 GACTACGTACCTACCAACCATGCGCATCTAG 1755
Db 1910 GACTACGTACCTACCAACCATGCGCATCTAG 1943

RESULT 3

ID ADO29096 standard; cDNA; 2694 BP.
XX ADO29096;
XX ADO29096;
DT 29-JUL-2004 (first entry)
XX Mouse novel GPCR GRM4 polynucleotide, SEQ ID NO:195.
DE G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cystostatic; antiinflammatory; vasotropic; antidiabetic; antidiarrhetic;
KW CNS; central nervous system; respiratory; antidiarrhetic; antidiabetic;
KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; gene; ss.
XX Mus musculus.
XX WO2004040000-A2.
PN 13-MAY-2004.
PD 09-SEP-2003; 2003WO-US028226.
PF 09-SEP-2003; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
PA Gaitanaris GA, Bergmann JE, Gragorov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI: 2004-390329/36.
DR P-PSDB; ADO29095.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 13; SEQ ID NO 195; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 2694 BP; 544 A; 866 C; 757 G; 527 T; 0 U; 0 Other;

Query Match 84.08; Score 1473.8; DB 12; Length 2694;
Best Local Similarity 92.2%; Pred. No. 2.8e-308;
Matches 1578; Conservative 0; Mismatches 97; Indels 36; Gaps 1;
Qy 42 AGGTTTCGACCGATATCTTCCAGCCGCGCAGCTGGACAAACAGGGCGCAATCTGGTT 101
Db 1020 AGGTTTCGACCGATATCTTCCAGCCGCGCAGCTGGACAAACAGGGCGCAATCTGGTT 1079
Qy 102 TGCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGGCCACGCTCAAGAGGG 161
Db 1080 TGCTGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCGGCCACGCTCAAGAGGG 1139
Qy 162 AGCCACATCAGAGTGCACCAACCGAGCGCATCGGCGAGGACTCGGCGCTATGAGCA 221
Db 1140 AAGCCACATCAGAGTGCACCAACCGAGCGCATCGGCGAGGACTCGGCGCTATGAGCA 1199
Qy 222 GGAGGGGAAGGTGCAGTTTCGTGATTGACGGTGTGTAGCCATGGGCGCAACGCTGCACGC 281
Db 1200 GGAGGGGAAGGTGCAGTTTCGTGATTGACGGTGTGTAGCCATGGGCGCAACGCTGCACGC 1259
Qy 282 CATGACCCGAGCTGTGTCCCGCGCGGTAGGACTCTGGCCTCGCATGAGACCCCGTGA 341
Db 1260 CATGACCCGAGCTGTGTCCCGCGCGGTAGGACTCTGGCCTCGCATGAGACCCCGTGA 1319
Qy 342 TGGCACCAGCTGCTTAAGTACATCAGAGAGTCAACTTCTCAGGSCATTCGGGGGAACCC 401
Db 1320 TGGCACCAGCTGCTTAAGTACATCAGAGAGTCAACTTCTCAGGSCATTCGGGGGAACCC 1379

Db 2646 CGGAGAGGCAAGTCTGAGCTTGGAGAACTTGGAGGCCCGCGCTGGCCACCAACA 2705
 QY 1722 GACCTACGTCACCTACCAACCAACGACCTGCTAG 1755
 Db 2706 GACTTACGTCACCTACCAACCAACGACCTGCTAG 2739

RESULT 5

AAAD38025
 ID AAD38025 standard; RNA; 3431 BP.
 XX
 AC AAD38025;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human metabotropic glutamate (mGluR4) receptor RNA.
 XX
 KW Human; metabotropic glutamate receptor; mGluR4; neurodegeneration;
 KW antipsychotic; anticonvulsant; analgesic; antidepressant; antiemetic;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 26..2764
 FT /*tag= a
 FT /product= "Human metabotropic glutamate receptor"
 XX
 FN US6384205-B1.
 XX
 PD 07-MAY-2002.
 XX
 PF 18-AUG-2000; 2000US-00641318.
 XX
 PR 12-MAR-1996; 96US-0013189P.
 PR 12-MAR-1997; 97US-00816178.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Belagaje RM, Wu S;
 XX
 XX WPI; 2002-442818/47.
 DR P-PSDB; AAE23757.
 XX
 PS New nucleic acid encoding human metabotropic glutamate receptor, useful
 PT e.g. in screening for specific agonists and antagonists for treating e.g.
 PT neurodegeneration.
 XX
 PS Claim 1; Col 23-26; 35pp; English.
 XX
 CC The present invention relates to human metabotropic glutamate receptor
 CC (mGluR4) proteins and polynucleotides encoding such proteins. Mglur4
 CC sequences of the invention are useful for treating acute and chronic
 CC neurodegeneration. They are also used as antipsychotic, anticonvulsant,
 CC analgesic, antidepressant and antiemetic agents. They are also useful for
 CC the diagnosis and/or treatment of conditions associated with an excess or
 CC deficiency of mGluR4. The present sequence is human mGluR4 RNA
 XX
 SQ Sequence 3431 BP; 648 A; 1128 C; 949 G; 0 T; 706 U; 0 Other;
 Query Match 83.8%; Score 1470.8; DB 6; Length 3431;
 Best Local Similarity 74.2%; Pred. No. 1.3e-307;
 Matches 1271; Conservative 291; Mismatches 152; Indels 0; Gaps 0;
 QY 42 AGGTTGACCAATCTCTCAGCGCGACGCTGGACAAACAGCGCGCAACATCTGTT 101
 Db 1051 AGGCUUCGACCGUACUUCUCCAGCGCGACGCGGACAAACACCGCGCGCAACUUCUGGU 1110
 QY 102 TCCCGAGTCTGGGAGGCAACTTCATTCGCAAGTTGAGCGCGCGCTCAAGAAGGG 161
 Db 1111 UGCGGAGUUCUGGGAGGCAACUUCGCAAGCUGAGCGCGCGCGCCUCCCAAGAAGGG 1170

QY 162 AAGCCACATCAAGAGTGCCACCAACGAGAGCGGCATCGGGCAGGACTCGGCCATATGACA 221
 Db 1171 CAGCCACUCUACAAGAGUGACCAACCGUGAGAAUUGGCGAGGAUUCAGCUAUUGAGA 1230
 QY 222 GGAGGGAAAGTGCAGTTGCGTATGACGCTGTGTACGCCATGGGCCACGCGCTGCACGC 281
 Db 1231 GGAGGGAAAGUGCAGUUUGUAGUAGCGGUGUACGCCAUGGGCCACGCGUGCAGCG 1290
 QY 282 CATGCACCGTGAACCTGTGTCGGCGCGGTAGGACTCTGCGCTCGCATGGACCCCGTGA 341
 Db 1291 CAUGCACCGUGACCUUGUCCGGCGGUGGGGUCUGCCGCGCGAUGGACCCUGAGA 1350
 QY 342 TGGCACCCAGCTGCTTAAGTATACAGGAACGTCAACTTCTCAGGCAATTCGGGGACCC 401
 Db 1351 UGGCACCCAGCTGCUUAAAGUAACUCCGAAACGUAACUUCUAGGCAUUGCGGGAACCC 1410
 QY 402 TGTAACTTCAATGAGAACGAGACGACCGGGGGCTACGACATCTACCACTACCAACT 461
 Db 1411 UUGACCUUCAAUGAAGUAGGAGUGCGCUGGGGCGUAGNACUACCAUACCAAGCU 1470
 QY 462 CGCCAATGGCTCGGCCGAGTAAAGGTCAATCGGCTCGTGGACAGACCACTCGACTCAG 521
 Db 1471 GCGCAACGAUUCUGCCGAGUACAAGGUCAUUGGCUCCUGGACUGACCACTCGACCUUAG 1530
 QY 522 AATGAGCGGATGCAATGTCGCCAGGAGTGGCCAGCAGCTGCGCGCTCATCTGCACTCT 581
 Db 1531 AAUAGAGCGGAGUACUGCGCGGGAGCGGCGAGCAGCGUGCGCCCGCUCUAGCAGCU 1590
 QY 582 GCCCTGCCAGCCCGGGAGCGAAGACACTGTGAAGGCGCATGGCTGCTGTCGACACTG 641
 Db 1591 GCCCUGCCACCGGGUGAGCGGAAGACAGUAGUAGGCGGCAUGCCUUGCUGGCGACUG 1650
 QY 642 CGAGCCCTGCACCGGGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCCCTA 701
 Db 1651 CGAGCTUUGCACAGGUAACAGUACCAAGUAGGACCGCUACACCTGUAAGAGCGUCCUA 1710
 QY 702 CGACATGCGGCCACAGAGAACCGGACAGCTGCCAGCCCATCCCATCTGCTCAAGTTGA 761
 Db 1711 UGACAUGCGGCCACAGAGAACCGGACGCGGCGGCGGCCAUCUCCCAUCAUACGCUGA 1770
 QY 762 GTGGAGCTCGCGCGTGGCGCGTGTGCTGCGCGTGGTGGGCATCGCGCCAC 821
 Db 1771 GUGGCGCUCGCGCCGUGGCGCGGCGCCUUCUUGCGCGGUGGUGGCAUGCGUCCAC 1830
 QY 822 GCTGTTCTGTGTGTGCTGCTGTGCGCTCAACAGATACCCCGCATCGTCAAGGCTCGGG 881
 Db 1831 GUUGUUCUGUGUACUACCUUUGUGGCUACAACGACACGCCCAUCUAGGCGUCCGG 1890
 QY 882 CCGGGAACGTGAGCTAGCTGCTGCTGGCGGCGATCTTTCTGTGCTACGCGCATCTCTCT 941
 Db 1891 CCGUGAACUGAGCUACGUGCUGGCGAGGCAUCUUCUGUGUAGUAGCCACCAUCCUCC 1950
 QY 942 CATGATCGCAGCGCGGACCTGCTGCTCGCGCGCATCTCTCTAGGCTCGG 1001
 Db 1951 CAUGAUCGUCAGCGCGGACCUUUGGCGCGGCGGCGGAAUUCUUCUGGAGUAGG 2010
 QY 1002 CATGAGCATGAGTACGCGCGCTGCTGACCAAGACCAACCGCATTTTACCGCATCTTTGA 1061
 Db 2011 GAUGAGCAUAGCUAUGCAGCGCCUGUCCACCAAGACCAACCGCAUACCGCAUUCGA 2070
 QY 1062 CGAGGGCAACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
 Db 2071 CGAGGGCAAGCGCUGGUGAGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2130
 QY 1122 CACCTTCATCTCATCTCTCTGAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1181
 Db 2131 CACCTTCATCTCATCTCTCTGAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2190
 QY 1182 CTCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
 Db 2191 CUCCCAUUGGUGGAGUAGUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2250
 QY 1242 CGTCTCAAGTGGCAATCTCGGACCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1301

[illegible]

Qy	1422	CCCCATCTTTTTGGGCACTCTCA	CAGT	CAGCGGAGCAAGCTGT	TATCATCCAGACCACT	1481
Db	2576	CCCCATCTTTTGGGCACTCTCG	CAGT	CGGCGGAGCAAGCTGT	TATCATCCAGACGACGCT	2635
Qy	1482	GACGGTCTCGTGGTCTGAGCG	CTTCA	GTGTCCTCGGAGATGCT	CTTACATGCCCCAAAGT	1541
Db	2636	GACGGTCTCGGTGAGTCTGAG	CGCCCT	CGGTGTCCCTTGGGAATGCT	CTTACATGCCCAAAGT	2695
Qy	1542	CTATCATCATCTCTTCCAC	CCCGGAGAGCAACGTG	CTCCAAAGCGCAAGCG	CAGCGCTCTCAAAGC	1601
Db	2696	CTATCATCATCTCTTCCAC	CCCGGAGAGCAACGTG	CTCCAAAGCGCAAGCG	CAGCGCTCTCAAAGC	2755
Qy	1602	CGTGGTCAACCGCGCCAC	CATGTC	CAACAAAGTTTCA	CAGAGAGGGCACTT	1661
Db	2756	CGTGGTCAACCGCGCCAC	CATGTC	CAACAAAGTTTCA	CAGAGAGGGCACTT	2815
Qy	1662	TGGGGAAGCCAAATCAG	AGCTGT	GTGAGAACCTG	TGAGGCCCGCGCTG	1721
Db	2816	CGAGAGGCCAAATCAG	AGCTGT	GTGAGAACCTT	TGAGGCCCGCGCTG	2875
Qy	1722	GACTACGTCACTACACCA	ACCATGCCATCTAG	1755		
Db	2876	GACTACGTCACTACACCA	ACCATGCCATCTAG	2909		
RESULT 8						
ID	ABZ42692	standard; DNA; 3884 BP.				
XX	ABZ42692;					
XX	04-MAR-2003 (first entry)					
XX	Human metabotropic glutamate receptor 4	nucleotide SEQ ID NO:175.				
XX	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;					
KW	G protein-coupled receptor modulator; antibody; immune-related disease;					
KW	growth-related disease; cell regeneration-related disease; AIDS; cancer;					
KW	immunological-related cell proliferative disease; autoimmune disease;					
KW	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;					
KW	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;					
KW	graft versus host disease; Parkinson's disease; multiple sclerosis; pain;					
KW	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;					
KW	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;					
KW	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;					
XX	ulcer; gene; ds.					
OS	Homo sapiens.					
XX	WO200261087-A2.					
XX	08-AUG-2002.					
XX	19-DEC-2001; 2001WO-US050107.					
XX	19-DEC-2000; 2000US-0257144P.					
XX	(LIFE-) LIFESPAN BIOSCIENCES INC.					
XX	Burmer GC, Roush CL, Brown JP;					
XX	WPI; 2003-046718/04.					
DR	P-PSDB; ABP81846.					
XX	New isolated antigenic peptides e.g., for G protein-coupled receptors					
PT	(GPCR), useful for diagnosing and designing drugs for treating conditions					
PT	in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or					
PT	autoimmune diseases.					
XX	Disclosure; Fig 1; 523pp; English.					
PS	The present invention describes antigenic peptides (I) comprising: (a)					
XX	any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino					
CC	sequences					

CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 3884 BP; 734 A; 1265 C; 1080 G; 805 T; 0 U; 0 Other;

Query Match 83.8%; Score 1470.8; DB 8; Length 3884;
Best Local Similarity 91.1%; Pred. No. 1.4e-307;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY	42	AGGTTTCAGCCGATCTTCTCAGCGCGCAGCGTGGACAAACAGCGCGCAACATCTGGTT	101
DB	1196	AGGCTTCAGCCGCTACTTCTCAGCGCGCAGCGTGGACAAACAGCGCGCAACATCTGGTT	1255
QY	102	TGCCAGTTCGGAGGACACTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAGGG	161
DB	1256	TGCCAGTTCGGAGGACACTTCCATGCAAGCTGAGCCGCCACGCGCTCAAGAGGG	1315
QY	162	AAGCCACATCAAGAGTGCACCAACGAGAGCGCATCGGGCAGGACTCGGCCATATGAGCA	221
DB	1316	CAGCCAGTCAAGAGTGCACCAACGCTGAGCGAATGGGCAAGATTGAGCTTATGAGCA	1375
QY	222	GGAGGGAGGTGCAGTTGCTGATTTGACGCTGTGTACGCGATGGGCGACGCGCTGACGC	281
DB	1376	GGAGGGAGGTGCAGTTTGTGATCGATCGCTGTACGCGATGGGCGACGCGCTGACGC	1435
QY	282	CATGCACCGTGACCTGTGTCGGCGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGA	341
DB	1436	CATGCACCGTGACCTGTGTCGGCGCGGTGGGGCTCTGCCCGCGCATGGACCCCTGTAGA	1495
QY	342	TGGCACCAGCTGCTTAAGTATACATCAGGAACGTCAACTTCTCAGGCATTTGGGGAAACC	401
DB	1496	TGGCACCAGCTGCTTAAAGTATACATCGAAGCGTCAACTTCTCAGGCATTTGGGGAAACC	1555
QY	402	TGTAACTTCAATAGAACGGAGACGCAACCGGGCGCTACGACATCTACCAAGTACCAACT	461
DB	1556	TGTGACCTTCAATAGAACGGAGATGCGCTGGGGCTATGACATCTACCAATACCAACT	1615
QY	462	GGCAATGGCTCGGCGGAGTACAAGGTCTATCGGCTCGTGGACAGACACCTGCACTCAG	521
DB	1616	GGCAATGGCTTTCGCGGAGTACAAGGTCTATGGCTCTGGAATGACCACTGCACTTAG	1675
QY	522	AATAGAGGGAGTGCAGTGGCCAGGAGTGGCCAGCAGCTGCCGCGCTCCATCTGCAGTCT	581
DB	1676	AATAGAGGGAGTGCAGTGGCCAGGAGTGGCCAGCAGCTGCCGCGCTCCATCTGCAGCT	1735
QY	582	GGCCTGCCAGCCCGGGAGCGAAAGAGATGTGTGAAGGCAATGGCTTGTCTGTCGCACTG	641
DB	1736	GGCCTGCCAGCCCGGGAGCGAAAGAGATGTGTGAAGGCAATGGCTTGTCTGTCGCACTG	1795
QY	642	CGAGCCCTGCACCGGGTACCAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTA	701
DB	1796	CGAGCCCTTGCA CAGGGTACCAGTACCAAGTGGACCGCTACACCTGTAAAGACCTGCCCTA	1855

QY	702	CGACATGCGGGCCACAGAGAACCGCACGAGCTGCCAGGCCATCCCATCGTCAAGTTGA	761
DB	1856	TGACATGCGGGCCACAGAGAACCGCACGAGCTGCCAGGCCATCCCATCGTCAAGTTGA	1915
QY	762	GTGGAGCTCGCGTGGGGCGGTGCTGCCCTCTTCTGCGCGGTGGGATCGCGCCAC	821
DB	1916	GTGGGGCTCGCGCTGGGGCGGTGCTGCCCTCTTCTGCGCGGTGGGATCGCGCCAC	1975
QY	822	GCTGTTCTGTTGGTGTGCTGCGCTTGTGCGCTACAAAGATACCCCATCGTCAAGGCTCGGG	881
DB	1976	GTTGTTCTGTTGGTGTGCTGCGCTTGTGCGCTACAAAGATACCCCATCGTCAAGGCTCGGG	2035
QY	882	CGGGAACTGAGCTACGCTGCTGCGGGGATCTTTCTGTGCTACGCGACCTACCTTCCT	941
DB	2036	CCGTGAACCTGAGCTACGCTGCTGCGGGGATCTTTCTGTGCTATGCGCACCTTCCT	2095
QY	942	CATGATCGCAGCGCGGACCTGGGACCTGTTGCTCGCGCGCATCTTCCTTAGGCTCGG	1001
DB	2096	CATGATCGCTGAGCGCGGACCTTGGCACCTGCTGCTGCGCGCAATCTTCCTGGGACTAGG	2155
QY	1002	CATGAGCATGAGCTACGCGGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTTGA	1061
DB	2156	GATGAGCATGAGCTATGAGCGCTGCTCACCAGACCAACCGCATTTACCGCATCTTTGA	2215
QY	1062	GCAGGGCAAAACGCTCGGTGCTGAGTGGCGCGCTTTCATGAGCGCGCTCGAGCTGGCCAT	1121
DB	2216	GCAGGGCAAGCGCTCGGTGCTGAGTGGCGCGCTTTCATGAGCGCGCTCGAGCTGGCCAT	2275
QY	1122	CACCTTCATCTCATCTCCCTGCGAGCTGCTCGGATCTCGGTGCTGGTGGGACCC	1181
DB	2276	CACCTTCAGCTCATCTCGCTGCGAGCTGCTGGGATCTGTGTGGTGGTGGGACCC	2335
QY	1182	CTCCACATCGGTGGTGGAGCTTCCAGGACCAACGACACTTGACCCCGCTTTGCCAGGGG	1241
DB	2336	CTCCACATCGGTGGTGGAGCTTCCAGGACCAACGAGGACACTCGACCCCGCTTTGCCAGGGG	2395
QY	1242	CGTCTCAAGTGCAGATCTCGGACCTGTCCTCATCTGCTGCTGCTGGGCTACAGATGCT	1301
DB	2396	TGTGCTCAAGTGTGACATCTCGGACCTGTCGCTCATCTGCTGCTGGGCTACAGATGCT	2455
QY	1302	GCTGATGTCAGGTGCTACTGTGATGCGCCATCAAGACCGAGCGGTGGCGGAGACTTCAA	1361
DB	2456	GCTCATGTCAGTGCACCGTGTATGCGCATCAAGACACGCGGCGGTGGCGGAGACTTCAA	2515
QY	1362	CGAGGCCAAGCCCATCGGCTTTCACCATGTACACCACTGCAATGCTGCTGGCTGCTCAT	1421
DB	2516	TGAGGCCAAGCCCATTTGGCTTTCACCATGTACACCACTGCAATGCTGCTGGCTGCTCAT	2575
QY	1422	CCCATCTCTTTTGGCACCTCAGCGACGACAGCTGTATCATCCAGAACCAACCACT	1481
DB	2576	CCCATCTCTTTTGGCACCTCAGCGAGTGGCGCGACAAAGCTGTATCATCCAGACGAGCT	2635
QY	1482	GACGCTCTCCGTGAGTCTGAGCGCTTCACTGCTCCCTGGGGATGCTCTATACGCCCAAGT	1541
DB	2636	GACGCTCTCCGTGAGTCTGAGCGCTTCACTGCTCCCTGGGGATGCTCTATACGCCCAAGT	2695
QY	1542	CTACATCATCTCTTTCACCCCGGAGCAAGCTGCGCCCAAGCGCAAGCGCAGTCTCAAAGC	1601
DB	2696	CTACATCATCTCTTTCACCCCGGAGCAAGCTGCGCCCAAGCGCAAGCGCAGTCTCAAAGC	2755
QY	1602	CGTGGTCAACCGCCGACCATGTCCAAAGTTTCAACAGAGTTTCAACAGAGGGCAACTTTCAGG	1661
DB	2756	CGTGGTCAACCGCCGACCATGTCCAAAGTTTCAACAGAGTTTCAACAGAGGGCAACTTTCAGG	2815
QY	1662	TGGGGAAGCCAAATCAGAGCTGTGTGAAACCTGGAGACCCGAGCGCTGGCTACCAACA	1721
DB	2816	CGGAGAGCCAAATCAGAGCTGTGTGAAACCTGGAGACCCGAGCGCTGGCTACCAACA	2875
QY	1722	GACCTAGCTACCTACCAACCAACCTGACCTAG	1755
DB	2876	GACTTACGCTACTTACCAACCAACCTGACCTAG	2909

Db 1916 GTGGGCTCGCCCTGGGCGGTGCTGCTCTCTCTGCGCGTGGGCATCGCTGCCAC 1975
Qy 822 GCTGTTGTTGGTGTACGTTTGTGGCTCAACGATACCCCATCGTCAAGGCTCGG 881
Db 1976 GTTGTGTTGGTGTACGTTTGTGGCTCAACGATACCCCATCGTCAAGGCTCGG 2035
Qy 882 CGGGAACTGAGTACGTTGCTGCTGGCGGATCTTTCTGTGCTACGCCACTTACCTTCT 941
Db 2036 CGTGAATGAGTACGTTGCTGCTGGCGGATCTTTCTGTGCTATGCCACACACTTCT 2095
Qy 942 CATGATCGAGACCGGACCTGGGACCTGTTGCTCGCGCGCATCTTCTTACGAGCTGG 1001
Db 2096 CATGATCGTGGCGCGGACCTGGGACCTGCTGCTGCGCGCAATCTTCTTGGGACTAG 2155
Qy 1002 CATGAGCATAGCTACGGGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTGA 1061
Db 2156 GATGAGCATAGCTATGAGCGCTGCTCACCAGACCAACCGCATTTACCGCATCTTGA 2215
Qy 1062 GCAGGCAACCGTGGTCACTGCGCCGCGCTTTTATCAGCCCGGCTCGCAGCTGGCCAT 1121
Db 2216 GCAGGCAAGCGCTGGTCACTGCGCCGCGCTTTTATCAGCCCGGCTCGCAGCTGGCCAT 2275
Qy 1122 CACCTTCATCTCATCTCCCTGCACTGCTCGGATCTGCGTGTGGTGTGCTGGGACCC 1181
Db 2276 CACCTTCAGCTCATCTCGCTGCACTGCTGGGATCTGCTGTGTGTTGTGTGGACCC 2335
Qy 1182 CTCACATCGGTGGTGGATCTTCAGGACCAACGAGACCTTGAACCCCGCTTTGGCAGGG 1241
Db 2336 CTCACATCGGTGGTGGATCTTCAGGACCAACGAGACCTTGAACCCCGCTTTGGCAGGG 2395
Qy 1242 CGTGTCAAGTGCGACATCTCGGACCTGCTCCTCATCTGCTGCTGGCTACACATGCT 1301
Db 2396 TGTGCTCAAGTGTGACATCTCGGACCTGCTCCTCATCTGCTGCTGGCTACACATGCT 2455
Qy 1302 GCTGATGTCACGTGTACTGTGTACGCTCAAGACCGGCGGTGCGGAGACCTTCAA 1361
Db 2456 GCTCATGTCACGTGTACGCTCAAGACCGGCGGTGCGGAGACCTTCAA 2515
Qy 1362 CGAGCCAAAGCCATCGGCTTACATGTACACACCTGATTTGCTGGCTGGCTTCAAT 1421
Db 2516 TGAGGCCAAAGCCATTTGGCTTACCATGTACACCACTTGCATCGTCTGGCTGGCTTCAAT 2575
Qy 1422 CCCCATCTTTTGGCACTCACAGTCAAGCTGACAGCTGTACATCCAGACCAACACACT 1481
Db 2576 CCCCATCTTTTGGCACTCGAGTGGCGGACCAAGCTGTACATCCAGACCAACAGCT 2635
Qy 1482 GACGCTCTCCGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGATGCTCTACATSCCAAGT 1541
Db 2636 GACGCTCTCCGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGATGCTCTACATSCCAAGT 2695
Qy 1542 CTACATCATCTCTTCCACCGGAGCAAGCTGCGCCAAAGGCGAAGCGAGCTCTCAAGC 1601
Db 2696 CTACATCATCTCTTCCACCGGAGCAAGCTGCGCCAAAGGCGAAGCGAGCTCTCAAGC 2755
Qy 1602 CGTGTACACCGCCGACCATGTCCAAAGTTCACAGAGGCGCACTTCAGGCCCAA 1661
Db 2756 CGTGTACACCGCCGACCATGTCCAAAGTTCACAGAGGCGCACTTCAGGCCCAA 2815
Qy 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAGAACTTGAGACCCCGCGCTGGCTTACCAACA 1721
Db 2816 CGGAGAGCCAAATCTGAGCTTGGAGAACTTGAGACCCCGCGCTGGCTTACCAACA 2875
Qy 1722 GACTTACGTACCTTACCAACCAATGCAATCTAG 1755
Db 2876 GACTTACGTACCTTACCAACCAATGCAATCTAG 2909

RESULT 11
AD156272 standard; DNA; 3884 BP.
XX AC AD156272;

XX 22-APR-2004 (first entry)
DT Human polynucleotide probe #1074.
XX
DE Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
XX effector-like polypeptide; cancer; immunopathology; neuropathology;
KW drug development; toxicology; carcinogenicity;
KW signalling pathway polypeptide; adrenal gland; bladder; bone;
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX Homo sapiens.
XX US2004010136-A1.
PN 15-JAN-2004.
XX 26-NOV-2002; 2002US-00305720.
XX 30-JAN-1998; 98US-00016434.
PR (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;
PI WPI; 2004-090520/09.
XX
DR New composition comprising polynucleotide probes, useful as array
XX elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
PT
XX Claim 6; SEQ ID NO 1074; 73pp; English.
PS
XX The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 3884 BP; 734 A; 1265 C; 1080 G; 805 T; 0 U; 0 Other;
Query Match 83.8%; Score 1470.8; DB 12; Length 3884;
Best Local Similarity 91.1%; Pred. No. 1.4e-307;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
Qy 42 AGGGTTCCAGCGGATCTTCTCCAGCGCGCATCTGGACAAACAGGGCGCAACATCTGTT 101
Db 1196 AGGCTTCGACGGCTACTTCTCCAGCGCGCATCTGGACAAACAGGGCGCAACATCTGTT 1255
Qy 102 TGCGGAGTTCTGGGAGGACAACTTCCATTTGAGCGCGCCCGCTCAAGAGGG 161

Db 1256 TCCGAGTTCTGGAGGACAACTTCCACTGCAAGCTGAGCCGCCACGCCCTCAAGAGGG 1315
Qy 162 AAGCCACATCAAGAAAGTGACCAACCGAGAGGCGCATCGGCGAGGACTCGGCCCTATGAGCA 221
Db 1316 CAGCCAGGTCAAGAAAGTGACCAACCGTGAGCGAATTGGGCAAGGATTACAGCTTATGAGCA 1375
Qy 222 GGAGGGGAAGTGCAAGTTGCTGATTTGACGCTGTGTACGCCATGGGCGCAGCGCTGACGC 281
Db 1376 GGAGGGGAAGTGCAAGTTGCTGATGCGATGCGCTGTGTACGCCATGGGCGCAGCGCTGACGC 1435
Qy 282 CATGACCGTGACCTGTGTCCCGGCGGTAGGACTCTGCCCTCGCATGGACCCCGTGA 341
Db 1436 CATGACCGTGACCTGTGTCCCGGCGGTGGGCTCTGCCCGCATGGACCCCTGTGA 1495
Qy 342 TGGCACCCAGCTGTCTAAGTATACATCAGGAACGTCAACTTCTCAGGCAATTGCGGGAAACC 401
Db 1496 TGGCACCCAGCTGTCTAAGTATACATCCGAAACGTCAACTTCTCAGGCAATCGCAGGAACC 1555
Qy 402 TGTAACTTCAATGAGAACGAGACGACCGGGGCGCTAGACATCTACAGTACCAACT 461
Db 1556 TGTGACCTTCAATGAGAAATGGAGATGCGCTGGGCGCTATGACATCTACCAATACCAGCT 1615
Qy 462 GCGCAATGCTCGGCGGAGTCAAGGTCAATCGGCTCGTGGACAGACCACTCACCCTGAG 521
Db 1616 GCGCAACGATCTGCGAGTCAAGGTCAATGGCTCTGGACTGACCACTGACCTTAG 1675
Qy 522 AATAGACGGATGCAAGTGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGTCT 581
Db 1676 AATAGACGGATGCAAGTGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAGCT 1735
Qy 582 GCCCTGCCAGCCCGGGAGCGAAAGAACTGTGAAGGCAATGGCTGTGTGTGGACATG 641
Db 1736 GCCCTGCCAACCGGGTGAGCGGAAGAAAGACAGTGAAGGCAATGGCTGTGTGTGGACATG 1795
Qy 642 CGAGCCCTGCACCGGTCACAGTCCAGTGAAGTGAACGCTACACCTGTAGACCTGCGCTA 701
Db 1796 CGAGCCCTTGCAACGGGTACAGTACAGTGAACGCTACACCTGTGAAGCAGTGTCCCTA 1855
Qy 702 GCACATGGGGCCACAGAGAACCGCACGAGCTGCCAGCCCATCCGCATCGTCAAGTTGA 761
Db 1856 TGACATGGGGCCACAGAGAACCGCACGAGCTGCCGGCCCATCCCATCATCAAGCTGA 1915
Qy 762 GTGGAATCGCGTGGGCGGTGCTGCCCTCTTCTGCGCGGTGGTGGGATCGCGCCAC 821
Db 1916 GTGCGGCTCGCGTGGGCGGTGCTGCCCTCTTCTGCGCGGTGGTGGGATCGCTGCCAC 1975
Qy 822 GCTGTTGCTGGTGCACGTTGTGCGCTACACGATACCCCATCGTCAAGGCGCTCGG 881
Db 1976 GTTGTGCTGGTGCACCTTTGTGCGCTACACGACAGCCCATCGTCAAGGCGCTCGG 2035
Qy 882 CCGGAACTGAGCTACGTGCTGCTGGCGGCACTTTTCTGTGCTACGCCACTACCTTCT 941
Db 2036 CCGTGAACGTGACTAGTGTGCTGCGAGGCACTTCTGTGCTATGCCACACCTTCT 2095
Qy 942 CATGATCGCAGAGCCGAGCTGGGACCTGTTGCTGCGCGCATCTTCTTAGGCTCGG 1001
Db 2096 CATGATCGTGAAGCCGACCTTGGACCTGCTGCTGCGCGCAATCTTCTCGGACTAGG 2155
Qy 1002 CATGAGCATCAGTACGCGGCGCTGCTGACCAAGACCAACCGCATTTACCGCATCTTGA 1061
Db 2156 GATGAGCATACGTATGACGCGCTGCTCACCAAGACCAACCGCATTTACCGCATCTTGA 2215
Qy 1062 CGAGGGCAAAAGCTGCGTCAAGTGGCGGTTTCTATCAGCCCGGCTCGCAGCTGGCAT 1121
Db 2216 CGAGGGCAAGCGCTGCTGCTGAGTGGCGGCTTCTATCAGCCCGGCTTACAGCTGGCAT 2275
Qy 1122 CACTTTCATCTCATCTCCCTGCAGCTGCTCGGCACTGCGGTGCTGTTGTTGGTGGACCC 1181
Db 2276 CACTTTCAGCTCATCTGCTGCAGCTGCTGGGCACTGCTGTTGTTGTTGGTGGACCC 2335
Qy 1182 CTCCCACTCGGTGGTGGATTCAGGACCAAGCGGACACTTGAACCCCGCTTGGCAGGG 1241
Db 2336 CTCCCACTCGGTGGTGGATTCAGGACCAAGCGGACACTCGACCCCGCTTGGCAGGG 2395

Qy 1242 CQTGCTCAAGTGCAGCATCTCGGACCTGTCCCTCATCTGCTGCTGCTGCTGCTGCTGCT 1301
Db 2396 TGTGCTCAAGTGTGACATCTCGGACCTGTGCTGCTCATCTGCTGCTGCTGCTGCTGCT 2455
Qy 1302 GCTGATGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1361
Db 2456 GCTCATGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2515
Qy 1362 CGAGCCCAAGCCCATCGGCTTCCACCATGTACACCACTGCTGCTGCTGCTGCTGCTGCT 1421
Db 2516 TGAGGCCAAGCCCATTTGCTTCCACCATGTACACCACTGCTGCTGCTGCTGCTGCT 2575
Qy 1422 CCCCATCTTTTGTGCACTCAGTCAAGCGGCAAGTGTATCATCCAGAACCACT 1481
Db 2576 CCCCATCTTTTGTGCACTCAGTCAAGCGGCAAGTGTATCATCCAGAACCACT 2635
Qy 1482 GACGCTCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
Db 2636 GACGCTCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2695
Qy 1542 CTACATCATCTTCCACCGGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601
Db 2696 CTACATCATCTTCCACCGGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2755
Qy 1602 CGTGCTACCGCGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1661
Db 2756 CGTGCTACCGCGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2815
Qy 1662 TGGGAAAGCCCAATCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1721
Db 2816 CCGAGAGCCCAAGTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2875
Qy 1722 GACCTACCTGCTACACCAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1755
Db 2876 GACTTACCTGCTACACCAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2909

RESULT 12

ADQ89113

ID ADQ89113 standard; cDNA; 3884 BP.

XX AC ADQ89113;

XX DT 21-OCT-2004 (first entry)

XX DE Human urological disorder related protein 115 encoding cDNA SEQ.65.

XX KW urological disorder; uropathic; cytostatic; urinary incontinence;

XX KW benign prostatic hyperplasia; human; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 171..2909

XX FT /*tag= a

XX FT /product= "urological disorder related protein 115"

XX FN WO2004065576-A2.

XX PD 05-AUG-2004.

XX PF 14-JAN-2004; 2004WO-US000750.

XX PR 15-JAN-2003; 2003US-0440318P.

XX PR 04-FEB-2003; 2003US-044783P.

XX PR 27-MAR-2003; 2003US-0457901P.

XX PR 08-MAY-2003; 2003US-0468775P.

XX PR 19-MAY-2003; 2003US-0471614P.

XX PR 16-JUN-2003; 2003US-0478742P.

XX PR 18-JUL-2003; 2003US-0488529P.

XX PR 30-JUL-2003; 2003US-0491156P.

XX PR 02-SEP-2003; 2003US-0499594P.

Db 2453 GCTCATGTACGTCACCGTGTATGCCATCAAGACACGCGCGTGCCTGAGACTTCAA 2512
 Qy 1362 CGAGCCAAAGCCCATCGCTTCAACATGTACACACCTGTCATTTGTCTGGCTGGCTTCAT 1421
 Db 2513 TGAGGCCAAAGCCCATTTGGCTTCAACATGTACACACCTGTCATCGTCTGGCTGGCTTCAT 2572
 Qy 1422 CCCCATCTTTTGGCACCTCACAGTCAGCCGACGCAAGCTGTACATCCACAGCAACACACT 1481
 Db 2573 CACCATCTTCTTTGGCACCTCGCAGTCGCGCGACAAAGCTGTACATCCACAGCAGACGCT 2632
 Qy 1482 GACGCTCTCCGTGAGTCTGAGCGCTTCAAGTGTCCCTGGGGATGTCTACATGCCCAAGT 1541
 Db 2633 GACGCTCTCGGTGAGTCTGAGCGCTCGTGTCTCCCTGGGATGTCTACATGCCCAAGT 2692
 Qy 1542 CTACATCATCTCTTCCACCGGAGAGCAAGCTGTCGCCCAAGGCGAAGCGCATCTCAAGC 1601
 Db 2693 CTACATCATCTCTTCCACCGGAGAGCAAGCTGTCGCCCAAGGCGAAGCGCATCTCAAGC 2752
 Qy 1602 CGTGTACCGCGCCGACCATGTCCAAAGTTCAACAGTTCAACAGAGGCAACTTCAGSCCAA 1661
 Db 2753 CGTGTACCGCGCGCCGACCATGTCCAAAGTTCAACAGTTCAACAGAGGCAACTTCAGSCCAA 2812
 Qy 1662 TGGGGAAGCCAAATCAGAGCTGTGTGAGAACTGTGAGAACCTGGAGACCCGCTGGCTACCAACA 1721
 Db 2813 CGGAGAGCCCAAGTCTGAGCTCTGGAGAACCTTGAGGCCCCGAGCGCTGGCCACCAACA 2872
 Qy 1722 GACTACGTCTACCTACACCAACCATGCGCATCTAG 1755
 Db 2873 GACTACGTCTACCTACACCAACCATGCAATCTAG 2906

RESULT 14

AAQ89342
 ID AAQ89342 standard; cDNA; 2738 BP.
 XX
 AC AAQ89342;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-SEP-1995 (first entry)
 XX
 XX
 DE Human mGluR4 cDNA.
 XX
 KW Human metabotropic glutamate receptor subtype 4; mGluR4; hmGluR4;
 KW signal transducer; ss.
 OS Homo sapiens.

OS
 FH Key Location/Qualifiers
 FT CDS 1..2738
 FT /*tag= a
 XX
 XX WO9508627-A1.
 XX
 XX 30-MAR-1995.
 XX
 XX 07-SEP-1994; 94WO-EP002991.
 XX
 XX 20-SEP-1993; 93EP-00810663.
 XX 19-AUG-1994; 94GB-00016553.
 XX
 XX (CIBA) CIBA GEIGY AG.
 XX
 XX Flor PJ, Kuhn R, Lindauer K, Puettner I, Knoepfel T;
 XX
 XX WPI; 1995-139596/18.
 XX P-PSDB; AAR72092.
 XX
 XX Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and 7 - also
 XX corresp. DNA and antibodies, useful for identifying cpds. which modulate
 XX signal transduction activity.
 XX
 XX Claim 17; Page 37-43; 110pp; English.

XX Human metabotropic glutamate receptor subtype 4 (hmGluR4) cDNA clones
 CC were isolated from a cerebellum cDNA library using a rat mGluR4 probe.
 CC Clone cmR20 lacked the 5' end of the hmGluR4 gene. PCR using human
 CC genomic or brain cDNA as template was used to obtain a complete gene
 CC sequence (given in AAQ89342) encoding hmGluR4 (AAR72092). Recombinant
 CC hmGluR4 was produced in mammalian cells. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 2738 BP; 545 A; 887 C; 783 G; 523 T; 0 U; 0 Other;
 Query Match 83.7%; Score 1468.2; DB 2; Length 2738;
 Best Local Similarity 91.1%; Pred. No. 4.6e-307;
 Matches 1560; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
 Qy 42 AGGTTTCAGCCGATCTTCTCCAGCCGACGCTGGACAAACAGAGCGCACATCTCGTT 101
 Db 1026 AGGTTTCAGCCGATCTTCTCCAGCCGACGCTGGACAAACAGAGCGCACATCTCGTT 1085
 Qy 102 TGGCGAGTTCTGGGAGGACAACTTCCATTTGCAAGTTGAGCGCGCCACCGCTCAAGAGGG 161
 Db 1086 TGGCGAGTTCTGGGAGGACAACTTCCATTTGCAAGTTGAGCGCGCCACCGCTCAAGAGGG 1145
 Qy 162 AAGCCACATCAAGAAGTGCACCAACCGAGAGCGCATCGGCGAGCACTCGGCTTATGACA 221
 Db 1146 CAGCCACGTCAAGAAGTGCACCAACCGTGAAGCAATTTGGGAGGATTCAGCTTATGACA 1205
 Qy 222 GGAGGGGAAGTGCAGTTCTGATTTGATGAGCTGTGTAGCCATGGCCATGGCCGCTGCACGC 281
 Db 1206 GGAGGGGAAGTGCAGTTCTGATTTGATGAGCTGTGTAGCCATGGCCATGGCCGCTGCACGC 1265
 Qy 282 CATGCACCGTGACCTGTCTCCGCGCGCTAGGACTCTGCCCTCGCATGGACCCCGCTGGA 341
 Db 1266 CATGCACCGTGACCTGTCTCCGCGCGCTGGGCTCTGCCCGCGCATGGACCCCTGTAGA 1325
 Qy 342 TGGCACCACGCTGTTAAGTACATCAGGAAAGCTCAACTTCTCAGGCAATTTGGGGGAACCC 401
 Db 1326 TGGCACCACGCTGTTAAGTACATCAGGAAAGCTCAACTTCTCAGGCAATTCGAGGGAACCC 1385
 Qy 402 TGTAACTTCAATGAGAACGGAGACGACCCGGGCGGTACGACATCTACCAAGTACCAACT 461
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 Qy 462 GCGCAATGGCTCGGCGCGAGTACAAAGTTCATCGGCTCGTGGAGACAGACCACTGCACCTCAG 521
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 Qy 762 GTGGGACTCGCGCTGGGCGCGTGTGCCCTTCTTCTGCGCGGTGGTGGGATCGCGGCCAC 821
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 Qy 822 GCTGTCTGT 881
 Db 1806 GTTGTCTGT 1865
 Qy 882 CCGGGAATGAGCTACGTTGCTGTGGGGGCACTTTTCTGTGTGTGTGTGTGTGTGTGTGTGT 941

Db 1866 CCGTGAACGTAGCTACGTGCTGCGCAGGATCTTCCTGTGCTATGCCACACCTTCT 1925
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Qy 1002 CATGACATCAGTACCGGCGCTGCTGACCAAGACCAACCGCATTTACGGCATCTTGA 1061
Db 1986 GATGACATCAGTATGACGCGCTGCTACCAAGACCAACCGCATTTACCGCATCTTGA 2045
Qy 1062 GCAGGCAAAACGGTCCGTGAGTCCGCGCTTTCATCAGCCGCGCTGCGAGTGGCCAT 1121
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Qy 1122 CACCTTCATCTCTCATCTCCCTGAGCTGCTGCGCATCTGCTGTGCTGCTGAGCC 1181
Db 2106 CACCTTCAGCTCATCTGCTGAGCTGCTGCGCATCTGCTGTGCTGCTGAGCC 2165
Qy 1182 CTCCTACTGCTGGTGGACTTCCAGGACCAACGGACACTTACCCCGCTTTCGCGAGGG 1241
Db 2166 CTCCTACTGCTGGTGGACTTCCAGGACCAACGGACACTTACCCCGCTTTCGCGAGGG 2225
Qy 1242 CTTGCTCAAGTGGACATCTCGACCTGCTCCCTCATCTGCTGCTGCTGCTGCTGCT 1301
Db 2226 TGTGCTCAAGTGGACATCTCGACCTGCTCCCTCATCTGCTGCTGCTGCTGCTGCT 2285
Qy 1302 GCTGATGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1361
Db 2286 GCTGATGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2345
Qy 1362 CGAGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
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Qy 1422 CCCCCTCTTTTGGCACTCTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 1481
Db 2406 CCCCCTCTTTTGGCACTCTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 2465
Qy 1482 GACGGTCTCGTGGTCTGAGGCTTTCAGTCTCCCTGCGGATGCTTACATGCCAAAGT 1541
Db 2466 GACGGTCTCGTGGTCTGAGGCTTTCAGTCTCCCTGCGGATGCTTACATGCCAAAGT 2525
Qy 1542 CTATCATCTCTTCCACCGGAGCAAGACGTGCGCAAGCGGAGCGGAGCTTCAAGC 1601
Db 2526 CTATCATCTCTTCCACCGGAGCAAGACGTGCGCAAGCGGAGCGGAGCTTCAAGC 2585
Qy 1602 CTTGCTCAGCGCGGACCATCTCCAAAGTTCACAGAGAGGGAAGTTCAGGCCCA 1661
Db 2586 CTTGCTCAGCGCGGACCATCTCCAAAGTTCACAGAGAGGGAAGTTCAGGCCCA 2645
Qy 1662 TGGGGAAGCAATCAGAGCTGTGTGAGAACCTTGGAGACCCAGCGCTGGTACCAACA 1721
Db 2646 CGAGAGGCAAGTCTGAGCTCTGCGAGAACCTTGGAGAACCTTGGAGAACCTTGGAG 2705
Qy 1722 GACCTACGTCTACCTACCAACCATGCTCTA 1754
Db 2706 GACTTACGTCTACCTACCAACCATGCTCTA 2738

RESULT 15
ADRO6667
ID ADRO6667 standard; cDNA; 3470 BP.
XX
AC ADRO6667;
XX
DT 04-NOV-2004 (first entry)
XX
DE Full length human cDNA useful for treating neurological disease Seq 173.
KW gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;

KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW tranquiliser.
OS Homo sapiens.
XX EP1447413-A2.
XX 18-AUG-2004.
XX 12-FEB-2004; 2004EP-00003145.
XX 14-FEB-2003; 2003JP-00102207.
XX 09-MAY-2003; 2003JP-00131452.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
XX Wakamatsu A, Ishii S, Nagai K, Irie R,
XX WPI; 2004-583265/57.
XX P-PSDB; ADR06623.
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX Claim 1; SEQ ID NO 173; 2686pp; English.
XX This invention relates to novel, isolated full length human cDNA
XX molecules and the encoded proteins thereof. Specifically, it refers to
XX cDNA clones obtained by an oligo-capping method, where none of these
XX clones are identical to any known human mRNAs. The present invention
XX describes an immunoassay to identify agonists and antagonists, as well as
XX antibodies, antisense molecules and siRNAs that can all be used to bind
XX to and modulate expression of the cDNA molecules. As such, these
XX molecules are useful for diagnostic markers or therapeutic targets for
XX the various diseases or morbid states. In particular, they are useful in
XX gene therapy for treating osteoporosis, neurological disease, Alzheimer's
XX disease, Parkinson's disease, dementia, short memory and various cancers,
XX as well as for maintaining equilibrium of sense or motor function, and
XX for treating emotional reaction, fear response and panic. Accordingly,
XX they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
XX cytostatic and tranquiliser activities. This polynucleotide is a full
XX length human cDNA sequence of the invention. NOTE: This sequence is not
XX given in the sequence listing of the specification but can be obtained on
XX CD-ROM from the European Patent Office, Vienna Sub-office.
SQ Sequence 3470 BP; 677 A; 1098 C; 935 G; 760 T; 0 U; 0 Other;

Query Match 81.1%; Score 1422.8; DB 13; Length 3470;
Best Local Similarity 90.9%; Pred. No. 3.1e-297;
Matches 1514; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
Qy 42 AGGGTTCCACCGATATCTTCAGCGCGCATCTGACCAACACAGCGCGCAACATCTGGTT 101
Db 580 AGGCTTCAGCGCTACTTCTCAGCGCGCATCTGACCAACACCGCGCGCAACATCTGGTT 639
Qy 102 TGCCGAGTTCTGGGAGGACAACTTCCATTGCAAGTTGAGCCGCCACGCGCTCAAGAAGG 161
Db 640 TGCCGAGTTCTGGGAGGACAACTTCCACTGCAAGTGAAGCGCGCGCTCAAGAAGG 699
Qy 162 AAGCCACATCAAGAGTGCACCAACCGAGAGCGCATCGGCGCAGAGTCTGGCCCTATGACA 221
Db 700 CAGCCACGTCAGAGTGCACCAACCGTGAAGTGGGCGAGGATTCAGCTTATGAGCA 759
Qy 222 GGAGGGGAAGTGCAGTTCGTGATGAGCTGTGTACGCCATGGGCCAGCGCTCAGCG 281
Db 760 GGAGGGGAAGTGCAGTTCGTGATGAGCTGTGTACGCCATGGGCCAGCGCTCAGCG 819
Qy 282 CATGCAACCGTGCACCTGTGTCGCGCGCGGTAGGACTCTGCCCTCGCATGGAACCCGTTGA 341
Db 820 CATGCAACCGTGCACCTGTGTCGCGCGCGGTGGGGCTCTGCCCGCGCATGGAACCCGTTGA 879
Qy 342 TGGCACCCAGCTGCTTAAGTATACAGGAACGTCAACTTCTCAGGCAATTGCGGGGAACCC 401

|||||
Db 880 TGGCACCAGCTGCTTAAGTACATCCGAAACGTCAACTTCTCAGGCATCGCGGAAACC 939
Qy 402 TGTAACTTTCAATGAGAACGGAGACGACCGGGGGCGCTACGACATCTTACCAAGTACCAACT 461
Db 940 TGTGACCTTCAATGAGAAATGGAGATGCGCTGGGGCGCTATGACATCTTACCAATACCAAGCT 999
Qy 462 GCGCAATGGCTCGGCGGAGTACAAGGTCAATCGGCTCGTGGACAGACACCACTGCAACCTCAG 521
Db 1000 GCGCAACGATTTGCGCGAGTACAAGGTCAATGGCTTCCTGGACTGACCACTGCAACCTTAG 1059
Qy 522 AATAGAGCGGATGCAAGTGGCCAGGAGTGGCCAGCAGCTGCGCGCTCCATCTGCAAGTCT 581
Db 1060 AATAGAGCGGATGCACTGGCCGGGAGCGGCGAGCAGCTGCGCGCTCCATCTGCAAGCT 1119
Qy 582 GCCCTGCCAGCCCGGGGACGGAAGAGAAGCTGTGGAAGGGCATGGCTTCTGCTGGCACTG 641
Db 1120 GCCCTGCCAACCAGGCTGAGCGGAAGAGACAGTGAAGGGCATGCTTGTCTGTGGCACTG 1179
Qy 642 CGAGCCCTGCCACCGGGTACCAAGTGGACCGCTACACCTGTAGACCTGCCCTTA 701
Db 1180 CGAGCCCTTGCACAGGGTACCAAGTGGACCGCTACACCTGTAGACCGTGTCCCTA 1239
Qy 702 CGACATGGGGCCACAGAGAACCGCACGAGCTGCCAGCCCATCCCCATCGTCAAGTTGGA 761
Db 1240 TGACATGGGGCCACAGAGAACCGCACGGGCTGCCGGCCATCCCCATCATCAAGTTGA 1299
Qy 762 GTGGACCTGCGCGTGGGCGTGTGCCCTCTTCTGCGCGTGGTGGGATCGCGGCCAC 821
Db 1300 GTGGGCTCGCGCTGGGCGTGTGCCCTCTTCTGCGCGTGGTGGGATCGCTGCCAC 1359
Qy 822 GCTGTCGTTGGTGCAGTGTGCGCTACAACGATACCCCATCGTCNAGGCTCGGG 881
Db 1360 GTTGTGCTGGTGATCACTTTGTGCGCTACAACGACACGCCCATCGTCAGGCGCTCGGG 1419
Qy 882 CGGGAACTGAGTACGTGCTGCTGGCGGGCATCTTCTGTGCTACGCCACTACCTTCT 941
Db 1420 CCGTGAACTGAGTACGTGCTGCTGGCAGGCATCTTCTGTGCTATGCCACCACTTCT 1479
Qy 942 CATGATCGCAGAGCCGAGCCTGGGACCTGTTGCTGCCGCGCATCTTCTTAGGGCTCGG 1001
Db 1480 CATGATCGCTGAGCCCGACCTTGGCACCCTGCTGCTGGCGCGAATCTTCTGGGACTAGG 1539
Qy 1002 CATGAGCATCAGTACGGGCCCTGCTGACCAAGACCAACCGCATTTACCGCATCTTGA 1061
Db 1540 GATGAGCATCAGTATGAGCCCTGCTCACCAGACCAACCGCATCTACCGCATCTTGA 1599
Qy 1062 GCAGGGCAAAACGGTCGGTCAGTGGCCCGGTTTCAATCAGCCCGGCTCGCAGCTGGCCAT 1121
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Qy 1122 CACCTTCAATCTCATCTCCCTGACGCTGCTGGGCATCTGCGTGGTGGTGGTGGACCC 1181
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Qy 1182 CTCACACTCGTGGTGGATTCAGGACCAAGGACATTCACCCCGGCTTGGCAGGG 1241
Db 1720 CTCACACTCGTGGTGGATTCAGGACCAAGGACATTCACCCCGGCTTGGCAGGG 1779
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Qy 1302 GCTGATGTCAGTGTATCTGTGTACGCGCATCAAGACCCGAGCGTGGCCGAGACCTTCAA 1361
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Qy 1362 CGAGGCCAAGCCCATCGGCTTACCATGTACACACCTGCTGCTGCTGGCTGGCTTCAAT 1421
Db 1900 TGAGGCCAAGCCCATTTGGCTTACCATGTACACACCTGCTGCTGCTGGCTGGCTTCAAT 1959
Qy 1422 CCCCATCTTTTGGCACCTCACAGTCAGCCGACACAGCTGTATCTCCAGACCAACCACT 1481
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Db 1960 CCCCATCTTCTTTGGCACCTCGCAGTCGGCGCAACAGCTGTATCATCCAGACGACGCGCT 2019
Qy 1482 GACGGTCTCGTGAATCTGAGCGCTTCAAGTGTCCCTGGGATGCTTACATGCCCAAGT 1541
Db 2020 GACGGTCTCGTGAATCTGAGCGCTTCAAGTGTCCCTGGGATGCTTACATGCCCAAGT 2079
Qy 1542 CTACATCATCTCTTCCACCGGAGCAGAAACGTGCGCCCAAGCGCAAGCGGCACTTCAAGC 1601
Db 2080 CTACATCATCTCTTCCACCGGAGCAGAAACGTGCGCCCAAGCGGCAAGCGGCACTTCAAGC 2139
Qy 1602 CGTGGTCAACCGCGCCACCATGTCCAAACAAAGTTCCACACAGAGGGCAACTTCAGGCCCAA 1661
Db 2140 CGTGGTCAACCGCGCCACCATGTCCAAACAAAGTTCCACACAGAGGGCAACTTCAGGCCCAA 2199
Qy 1662 TGGGAAAGCCAAATCAGAGCTGTGTGAGAACCTTGGACACCCCGCG 1707
Db 2200 CGGAGAGGCCAAAGTCTGAGCTTGGAGAACCTTGGAGGCCCGCGG 2245

Search completed: June 21, 2005, 05:02:17
Job time : 999 secs

GenCore version 5.1.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 01:57:35 ; Search time 7720 Seconds
(without alignments)
11015.402 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 1755

Sequence: 1 atgccagggtatcatc.....acaccaacatgccatctag 1755

Scoring table:

IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1712.4	97.6	4488	10	RATMGLUR4A
2	1707.6	97.3	2838	6	AR381454
3	1707.6	97.3	3704	10	RATMGLURBD
4	1560.4	88.9	4425	10	BC072635
5	1516.4	86.4	3868	10	RNU47331
6	1470.8	83.8	3176	9	AK122982
7	1470.8	83.8	3431	6	AR208972
8	1470.8	83.8	3431	9	HSU92457
9	1470.8	83.8	3850	9	AK122836
10	1470.8	83.8	3884	6	AR6196
11	1470.8	83.8	3884	6	AR270511
12	1470.8	83.8	3884	6	AR381464
13	1470.8	83.8	3884	6	AX548890
14	1470.8	83.8	3884	6	AX548890
15	1470.8	83.8	3884	6	AX548890
16	1470.8	83.8	3884	9	HSWGLUR4
17	1469.8	83.7	2738	6	A43637
18	1469.8	83.7	2738	6	AX427263
19	1467.8	83.6	2736	6	AR149574

20	1422.8	81.1	3470	6	CQ849704	Sequence
21	1422.8	81.1	3470	9	AK126746	AK26746 Homo sapi
22	1340.6	76.4	3590	6	CQ853450	Sequence
23	1340.6	76.4	3590	9	AK131536	AK131536 Homo sapi
24	1331.2	75.9	2548	6	CQ730036	Sequence
25	1281.4	73.0	3002	10	BC080284	BC080284 Mus muscu
26	935.8	53.3	221062	2	AC134369	AC134369 Rattus no
27	916	52.2	2041	5	AB042755	AB042755 taenlopyg
28	880.6	50.2	2961	6	AR071655	AR071655 Sequence
29	880.6	50.2	2961	6	AR202435	Sequence
30	880.6	50.2	6122	6	AX548894	AX548894 Sequence
31	871	49.6	2670	6	AR106168	AR106168 Sequence
32	860.2	49.0	2635	6	AR106169	Sequence
33	859.8	49.0	2727	10	AY673682	AY673682 Mus muscu
34	855	48.7	2793	10	RNU63288	U63288 Rattus norv
35	851.8	48.5	2830	6	AX418281	AX418281 Sequence
36	851.8	48.5	2830	10	MMU17252	U17252 Mus musculu
37	849	48.4	213609	10	AC127341	AC127341 Mus muscu
38	843.8	48.1	3212	4	AY275542	AY275542 Oryctolopg
39	842.2	48.0	2727	9	HSU95025	U95025 Homo sapien
40	839	47.8	3321	6	AR147650	AR147650 Sequence
41	839	47.8	3321	6	AR147651	Sequence
42	839	47.8	3321	6	AX548898	AX548898 Sequence
43	839	47.8	3321	6	AX658362	AX658362 Sequence
44	839	47.8	3321	9	HSU92459	U92459 Human metab
45	833.2	47.5	4418	10	RATMGLUR6	D13963 Rattus norv

ALIGNMENTS

RESULT 1	RATMGLUR4A	4488 bp	mRNA	linear	ROD 01-APR-1996
LOCUS	Rat metabotropic glutamate receptor (GLUR4)	mRNA	complete cds.		
DEFINITION	M90518				
ACCESSION	M90518.1	GI:205400			
VERSION	Metabotropic glutamate receptor.				
KEYWORDS	Rattus norvegicus (Norway rat)				
SOURCE	Rattus norvegicus				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 4488)				
AUTHORS	O'Hara,P.J., Sheppard,P.O., Thøgersen,H., Venezia,D., Haldeman,B.A., McGrane,V., Houamed,K.M., Thomsen,C., Gilbert,T.L. and Mulvihill,E.R.				
TITLE	The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins				
JOURNAL	Neuron 11 (1), 41-52 (1993)				
MEDLINE	93332699				
PUBMED	8338667				
REFERENCE	2 (bases 1 to 4488)				
AUTHORS	O'Hara,P.J.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-APR-1992) Patrick J. O'Hara, ZymoGenetics, Inc., Seattle, WA 98105, USA				
COMMENT	Original source text: Rattus norvegicus cDNA to mRNA.				
FEATURES	Location/Qualifiers				
source	1..4488				
	/organism="Rattus norvegicus"				
	/mol_type="mRNA"				
	/db_xref="taxon:10116"				
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	1..4488				
	/gene="GLUR4"				
gene	1..4488				
mRNA	/gene="GLUR4"				
CDS	855..3593				
	/gene="GLUR4"				
	/note="putative"				
	/codon_start=1				
	/product="metabotropic glutamate receptor"				

VERSION	AR381454.1	GI:40089512
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 2838)	
AUTHORS	Chaudhari,N. and Roper,S.D.	
TITLE	Taste receptor for umami (monosodium glutamate) taste	
JOURNAL	Patent: US 6608176-A 1 19-AUG-2003;	
FEATURES	Location/Qualifiers	
source	1..2838	
	/organism="unknown"	
	/mol_type="genomic DNA"	
ORIGIN		
Query Match	97.3%;	Score 1707.6; DB 6; Length 2838;
Best Local Similarity	99.8%;	Pred. No. 1.5e-272;
Matches 1710;	Conservative 0;	Mismatches 4; Indels 0; Gaps 0;
QY	42	AGGGTTGACCGCATCTCTCAGCGCGCACGCTGGACAAACAGCGCGCAACATCTGGTT 101
Db	230	AGGGTTGACCGCATCTCTCAGCGCGCACGCTGGACAAACAGCGCGCAACATCTGGTT 289
QY	102	TGCCAGTCTGGAGGACAACTTCCATTGCAAGTTGAGCCGCCAGCGCTCAAGAAGG 161
Db	290	TGCCAGTCTGGAGGACAACTTCCATTGCAAGTTGAGCCGCCAGCGCTCAAGAAGG 349
QY	162	AAGCCACATCAAGAAGTGACCAACCGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCA 221
Db	350	AAGCCACATCAAGAAGTGACCAACCGAGAGCGCATCGGGCAGGACTCGGCCCTATGAGCA 409
QY	222	GGAGGGGAAGTGCAAGTTGTAAGCTGTGTACGCAATGGGCCACGCGCTGCACGC 281
Db	410	GGAGGGGAAGTGCAAGTTGTAAGCTGTGTACGCAATGGGCCACGCGCTGCACGC 469
QY	282	CATGACCGTGACCTGTGTCCCGCGCGGTAGGACTCTGCCCTCGATGGACCCCGTGA 341
Db	470	CATGACCGTGACCTGTGTCTGGCGCGGTAGGACTCTGCCCTCGATGGACCCCGTGA 529
QY	342	TGGCACCAGCTGCTTAAGTATACAGGAACGTCAACTTCTCAGGCATTTGGGGGAACCC 401
Db	530	TGGCACCAGCTGCTTAAGTATACAGGAACGTCAACTTCTCAGGCATTTGGGGGAACCC 589
QY	402	TGTAACCTTTCAATGAGACGGAGACGACCGGGGCGCTACGACATCTACCAAGTACCAACT 461
Db	590	TGTAACCTTTCAATGAGACGGAGACGACCGGGGCGCTACGACATCTACCAAGTACCAACT 649
QY	462	GGGCAATGGCTCGGCGGAGTACAAGGTCAATCGGCTCGTGGACAGACCACTGCACCTAG 521
Db	650	GGCCAATGGCTCGGCGGAGTACAAGGTCAATCGGCTCGTGGACAGACCACTGCACCTAG 709
QY	522	AATAGACGGGATGCAGTGGCCAGGAGTGGCCAGCAGCTGCCGCGCTCCATCTGCAGTCT 581
Db	710	AATAGACGGGATGCAGTGGCCAGGAGTGGCCAGCAGCTGCCGCGCTCCATCTGCAGTCT 769
QY	582	GCCTGCCACCGCGGGGCGGAAAGAACTGTGAAGGCGATGGCTTGTCTGTGGCACTG 641
Db	770	GCCTGCCACCGCGGGGCGGAAAGAACTGTGAAGGCGATGGCTTGTCTGTGGCACTG 829
QY	642	CGAGCCCTGACCGGGTACCAAGTACAAGTGAACCGCTACCTGTGAAGACCTGCCCTTA 701
Db	830	CGAGCCCTGACCGGGTACCAAGTACAAGTGAACCGCTACCTGTGAAGACCTGCCCTTA 889
QY	702	GCACATGGGGCCACAGAGAACCGCACGAGCTGCCAGCCCATCCCATCGTCAAGTTGA 761
Db	890	GCACATGGGGCCACAGAGAACCGCACGAGCTGCCAGCCCATCCCATCGTCAAGTTGA 949
QY	762	GTGGAGCTCGCGGTGGCGCTGCTGCCCTCTTCTGCGCGGTGGGCGATCGCGCCAC 821
Db	950	GTGGAGCTCGCGGTGGCGCTGCTGCCCTCTTCTGCGCGGTGGGCGATCGCGCCAC 1009
QY	822	GCTGTTCTGGTGGTCAAGTTTGTGCGCTTACCAAGATACCCCATCGTCAAGCGCTCGGG 881

Db	1010	GCTGTTCTGGTGGTACAGTTTGTGGCTACACGATACCCCATCGTCAAGCCCTCGGG 1069
QY	882	CCGGAACTGAGCTACGTGCTGGCGGGCATCTTTCTGTGCTACGCCACTACTTCTCT 941
Db	1070	CCGGAGCTGAGCTAGCTGCTGGCGGGCATCTTTCTGTGCTACGCCACTACTTCTCT 1129
QY	942	CATGATCGCAGACCGGACCTGGGACCTGTTCGCTCGCGCGCATCTTCTTAGGGCTCGG 1001
Db	1130	CATGATCGCAGACCGGACCTGGGACCTGTTCGCTCGCGCGCATCTTCTTAGGGCTCGG 1189
QY	1002	CATGAGCATGAGCTACGCGGCGCTGTCACCAAGACCAACCGCATTTACCGCATCTTTGA 1061
Db	1190	CATGAGCATGAGCTACGCGGCGCTGTCACCAAGACCAACCGCATTTACCGCATCTTTGA 1249
QY	1062	GCAGGGCAACCGTGGTCAAGTGGCCCGCTTTTCATCAGCCCGGCTCGCAGCTGGCCAT 1121
Db	1250	GCAGGGCAACCGTGGTCAAGTGGCCCGCTTTTCATCAGCCCGGCTCGCAGCTGGCCAT 1309
QY	1122	CACCTTCATCTCATCTCCCTGCGAGCTGCTCGGCATCTCGGTGTGGTTCGTGGTGACCC 1181
Db	1310	CACCTTCATCTCATCTCCCTGCGAGCTGCTCGGCATCTCGGTGTGGTTCGTGGTGACCC 1369
QY	1182	CTCCCACTCGGTGGTGGACTTCCAGGACCAACCGACACTTGACCCCGCTTTGCCAGGG 1241
Db	1370	CTCCCACTCGGTGGTGGACTTCCAGGACCAACCGACACTTGACCCCGCTTTGCCAGGG 1429
QY	1242	CGTGCTCAAGTGGCAGCATCTCGGACCTGCTCCCTCATCTGCTGCTGGGCTACAGCATGCT 1301
Db	1430	CGTGCTCAAGTGGCAGCATCTCGGACCTGCTCCCTCATCTGCTGCTGGGCTACAGCATGCT 1489
QY	1302	GCTGATGTGCTAGTGTACTGTAGCGCATCAAGACCCGAGCGGTGCCGAGACCTTCA 1361
Db	1490	GCTGATGTGCTAGTGTACTGTAGCGCATCAAGACCCGAGCGGTGCCGAGACCTTCA 1549
QY	1362	CGAGCCCAAGCCCATCGGCTTTCACCATGTACACCACTGATGCTGCTGGCTGCTCAT 1421
Db	1550	CGAGCCCAAGCCCATCGGCTTTCACCATGTACACCACTGATGCTGCTGGCTGCTCAT 1609
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QY	1482	GACGCTCTCCGTAGTCTGAGCGCTTCAAGTGTCCCTGGGGATGCTCTACATGCCCAAGT 1541
Db	1670	GACTGTCTCCGTAGTCTGAGCGCTTCAAGTGTCCCTGGGGATGCTCTACATGCCCAAGT 1729
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Db	1910	GACCTACGTCACCTACCAACCATGCCATCTAG 1943
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LOCUS	RATMGLURBD	3704 bp mRNA linear ROD 27-APR-1993
DEFINITION	Rat metabotropic glutamate receptor 4 mRNA, primary transcript.	
ACCESSION	M92077	
VERSION	M92077.1	GI:205403
KEYWORDS	glutamate receptor; metabotropic glutamate receptor.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

BC072635.1	GI:49257159	Mus musculus (house mouse)	
Mus musculus		Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klauener,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshuler,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F., Dotchenko,L., Marudina,K., Farmer,A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schreitz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carminci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bonasak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.			
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
12477932			
2 (bases 1 to 4425)			
Strausberg,R.			
Direct Submission			
Submitted (03-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
NIH-MGC Project URL: http://mgc.nci.nih.gov			
Contact: MGC help desk			
Email: cgapbs-r@mail.nih.gov			
Tissue Procurement: Dr. Jim Lin, University of Iowa			
cDNA Library Preparation: M. Bento Soares, University of Iowa			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.			
Web site: http://genome.uiowa.edu			
Contact: bento-soares@uiowa.edu ; tom-casavant@uiowa.edu			
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fisher,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J., Casavant,T., Soares,M.B.			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			
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Series: Plate: Row: Column: 0.			
Location/Qualifiers			

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RESULT 5
RNU47331 3868 bp mRNA linear ROD 16-OCT-2002
LOCUS Rattus norvegicus metabotropic glutamate receptor 4b mRNA, complete cds.
DEFINITION
ACCESSION U47331
VERSION U47331.1 GI:1197725
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ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
REFERENCE 1 (bases 1 to 3868)
AUTHORS O'Hara, P.J.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1996) Patrick J. O'Hara, ZymoGenetics, 1201 Eastlake Avenue East, Seattle, WA 98102, USA
LOCATION/Qualifiers
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ORIGIN

Query Match 86.4%; Score 1516.4; DB 10; Length 3868;
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Matches 1517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1880 AGGTTTCGACGATATCTTCCAGCCGACGCTGGACAAACAGAGGCGCAACTCTGGTT 1939
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Db 1940 TGGCGAGTTTCGGAGGACAACTTCCATTCGAGTTCGAGCGCCGACCGCTCAAGAGGG 1999
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Qy 342 TGGCACCCAGCTGCTTAAGTACATCAGGAAAGTCAACTTCTCAGGCAATTCGGGGAACCC 401
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DEFINITION Sequence 1 from patent US 6384205.
ACCESSION AR208972
VERSION AR208972.1 GI:21510266
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3431)
AUTHORS Belagaje, R.M. and Wu, S.
TITLE Metabotropic glutamate receptor 4 nucleic acid
JOURNAL Patent: US 6384205-A 1 07-MAY-2002;
FEATURES
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Query Match 83.8%; Score 1470.8; DB 6; Length 3431;
Best Local Similarity 91.1%; Pred. No. 2e-233;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Qy 42 AGGGTTCGACCGGATCTTCTCCAGCGCCAGCTGGACAAACAGGCGCAACATCTGTT 101
Db 1051 AGGCTTCGACCGGATCTTCTCCAGCGCCAGCTGGACAAACAGGCGCAACATCTGTT 1110
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DB 1891 CCGTGAATGAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1950
QY 942 CATGATCGCAGCGGACCTGGGACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1001
DB 1951 CATGATCGTGAAGCCGACCTTGGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2010
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RESULT 8
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DEFINITION Sequence 3 from patent US 6384205.
ACCESSION AR208973
VERSION AR208973.1 GI:21510267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3431)
AUTHORS Belagaje,R.M. and Wu,S.
TITLE Metabotropic glutamate receptor 4 nucleic acid
JOURNAL Patent: US 6384205-A 3 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..3431
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Query Match 83.8%; Score 1470.8; DB 6; Length 3431;
Best Local Similarity 91.1%; Pred. No. 2e-233;
Matches 1562; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 42 AGGGTTCCAGCGATCTTCTCCAGCGCAGCTGGACAAACAGAGCGCAACATCTGGTT 101
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DB 1111 TGCCGAGTTCTGGGAGGACAACTTTCATTTGCAAGTTGAGCCGCCACGCGCTCAAGAACGG 1170
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DB 1171 CAGCCACGTCAAGAAAGTGCACCAACCGAGAGCGCATCGGCGAGGACTCGGCTATGACA 1230
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ACCESSION U92457
VERSION U92457.1 GI:1935038
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3431)
AUTHORS Wu, S., Wright, R.A., Rockey, P.K., Burgett, S.G., Arnold, J.S.,
Roetck, P.R. Jr., Johnson, B.G., Schoepf, D.D. and Belagaje, R.M.
TITLE Group III human metabotropic glutamate receptors 4, 7 and 8:
molecular cloning, functional expression, and comparison of
pharmacological properties in RGT cells
JOURNAL Brain Res. Mol. Brain Res. 53 (1-2), 88-97 (1998)
MEDLINE 98141892
PUBMED 9473604
REFERENCE 2 (bases 1 to 3431)
AUTHORS Wu, S. and Belagaje, R.M.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-1997) mc625, Eli Lilly and Company, Lilly
Corporate Center, Indianapolis, IN 46285, USA
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1122	Qy	CACCTTCATCTCATCTCCCTGACGCTGCTCGGCATCTGCGTGTGGTTCGTGTGTGACCC	1181
2276	Db	CACCTTCAGCCTCATCTCGCTGCGAGCTGCTGGGCATCTGTGTGTGTTGTGTGTGACCC	2335
1182	Qy	CTCCACTCTGGTGGTGAATTCACGAGCAACCGGACACTTGTACCCCGCTTTGCCAGGGG	1241
2336	Db	CTCCACTCGTGGTGGACTTCCAGGACCAAGCGGACACTCGACCCCGCTTCGCGAGGGG	2395
1242	Qy	CGTGCTCAAGTGGCAGACATCTCGGACCTGTCCCTCATCTGCTGCTGGCTTACAGCATGCT	1301
2396	Db	TGTGCTCAAGTGTGACATCTCGGACCTGTGCTCATCTGCTGCTGGGCTTACAGCATGCT	2455
1302	Qy	GCTCATGGTCACTGCTGATCTGTGTACGGCCATCAAGACCCGAGGGCGTGCCGAGACCTTCAA	1361
2456	Db	GCTCATGGTCACTGCTGACCGTGTATGTCATCAAGACACGGCGTGCCGAGACCTTCAA	2515
1362	Qy	CGAGGCCAAGCCCATCGGCTTCAACATGTACACCACTGATGTCTGTGGCTGGCCTTCAT	1421
2516	Db	TGAGGCCAAGCCCATTGGCTTCAACATGTACACCACTGTCATCGTCTGGCTGGCCTTCAT	2575
1422	Qy	CCCCATCTTTTGGCACCTCAGAGTCAGCGGACGAAGCTGTACATCAGACACACCACT	1481
2576	Db	CCCCATCTTCTTTGGCACCTCGCAGTGGCGGACGAAGCTGTACATCAGACGACGACGCT	2635
1482	Qy	GACGGTCTCCGTGAGTCTGAGCGCTTCAGTGTCCCTGGGGATGCTCTACATGCCCCAAGT	1541
2636	Db	GACGGTCTCCGTGAGTCTGAGCGCTCGTGTCCCTGGGAATGCTCTACATGCCAAGT	2695
1542	Qy	CTACATCATCTCTTCCACCGGAGCAGAACGTGCCCAAGCGCAGCGCATCTCAAAGC	1601
2696	Db	CTACATCATCTCTTCCACCGGAGCAGAACGTGCCCAAGCGCAGCGCATCTCAAAGC	2755
1602	Qy	CGTGGTCAACCGCGCCACCATGTCCACACAGTTCCACAGAAGGGCACTTCAGGCCCAA	1661
2756	Db	CGTGGTTCAGCGCGGCCACCATGTCCACACAGTTCCACGAGAAGGGCACTTCAGGCCCAA	2815
1662	Qy	TGGGGAAAGCCAAATCAGAGCTGTGTGAGAACCTCGAGACCCCGCGTGTGCTACCAACA	1721
2816	Db	CGGAGAGCCCAAGTCTGAGCTCTGCGAGAACCTTGAGGCCCGCAGCGTGGCCCAACA	2875
1722	Qy	GACCTAGCTCACCTTACACCAACCATGGCAATCTAG	1755
2876	Db	GACTTAGTCACTTACACCAACCATGCAATCTAG	2909

RESULT 12					
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LOCUS	AR270511	3884 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	Sequence 1074 from patent US 6500938.				
ACCESSION	AR270511				
VERSION	AR270511.1	GI:29701745			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 3884)				
TITLE	Au-Young,J. and Seilhamer,J.J.				
	Composition for the detection of signaling pathway gene expression				

Db	2096	CATGATCGCTGAGCCCGA	CTTGTGGCACTGTGCTGGCGCCGAATCTTCTCTGGGAGCTAGG	2155
Qy	1002	CATGAGCATCAGCTACGCGCCCTGCTGACCAAGACCAACCGCATTTTACCAGCTCTTGA	1061	
Db	2156	GATGAGCATCAGCTATGACGCTCTGTCTACCAAGACCAACCGCATTTACCAGCTCTTGA	2215	
Qy	1062	GCAGGGCAAAACGCTGCGGTGAGTGCCCGCGTTTCATATCAGCCCGGCTCGCAGCTGGCCAT	1121	
Db	2216	GCAGGGCAAGCGCTCGGTGAGTGCCCGCGTTTCATATCAGCCCGGCTCACAGCTGGCCAT	2275	
Qy	1122	CACCTTCATCTCATCTCCCTGAGCTGCTCGGCATCTGCGTGTGGTTCGTGGTGAGCC	1181	
Db	2276	CACCTTCAGCTCATCTCGCTGAGCTGCTGGGCATCTGTGTGTGGTGTGTGTGGAGCC	2335	
Qy	1182	CTCCACTCGGTGGGACTTCCAGAGCAACAGCACTTGACCCCGCGTTTGGCAGGG	1241	
Db	2336	CTCCACTCGGTGGGACTTCCAGAGCAACAGCGGACATCTGNACCCCGCTTGCAGGG	2395	
Qy	1242	CGTGCTCAAGTGGCAATCTCGGACCTGTCCCTCATCTGCTGCTGGGCTACAGACTCT	1301	
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Qy	1302	GCTGATGGTCAGTGTACTGTGTAGCCCATCAAGACCCGAGCGGTGCCGAGACTTCAA	1361	
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Qy	1362	CGAGGCAAGCCCATCGGCTTCAACATGTACACCACTTGCAATGTCTGGCTGGGCTTCAT	1421	
Db	2516	TGAGGCAAGCCCATTTGGCTTCAACATGTACACCACTTGCAATGTCTGGCTGGGCTTCAT	2575	
Qy	1422	CCCCATCTTTTGGCACCTCACTGACGCGCAAGCTGTATCATCCAGACAACCACT	1481	
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Qy	1482	GACGCTCGGTGAGTCTGAGCGCTTCACTGTCTCCCTGGGGATGTCTTACATGGCCAAAGT	1541	
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Qy	1662	TGGGGAAGCCAAATCAGAGCTGTGTAGAACCTCGAGACCCGAGCGCTGGGTACAAACA	1721	
Db	2816	CGGAGAGGCGAAGTCTGAGCTCTGGGAGAACCTTGGAGCGCCGAGCGCTGGCCACCAACA	2875	
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LOCUS				
Sequence 14 from patent US 6608176.				
AR381464				
ACCESSION				
VERSION				
AR381464.1				
GI:40089522				
KEYWORDS				
Unknown.				
SOURCE				
ORGANISM				
Unclassified.				
REFERENCE				
1 (bases 1 to 3884)				
AUTHORS				
Chaudhari, N. and Roper, S.D.				
TITLE				
Taste receptor for umami (monosodium glutamate) taste				
JOURNAL				
Patent: US 6608176-A 14 AUG-2003;				
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Location/Qualifiers				
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ORIGIN	Query Match	83.8%	Score 1470.8;	DB 6;	Length 3884;
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Qy	42	AGGGTTTCGACCGATACTTCTCCAGCCGCA	CGCTGCGACCAACAAAGGCGCAACATCTCGTT	101	
Db	1196	AGGCTTCGACCGCTACTTCTCCAGCGCG	CTGCGACAAACAACCGCGCAACATCTCGTT	1255	
Qy	102	TGCCAGTCTTGGGAGGACAACTTCCATTG	CAATTGCAAGTTGAGCGGCACACCGCTCAAGAAGG	161	
Db	1256	TGCCAGTCTTGGGAGGACAACTTCCATTG	CAATTGCAAGTTGAGCGGCACACCGCTCAAGAAGG	1315	
Qy	162	AAGCCACATCAAGAAGTGCACCAACCGAG	AGCGCATCGGCGAGGACTTCGCGCTTATGACA	221	
Db	1316	CHGCCACGTCAAGAAGTGCACCAACCGT	AGCGAATTTGGGAGGATTTACGCTTATGACA	1375	
Qy	222	GGAGGGAGGTGCGATTGCGTGTGATGTAG	CGCTGTGTACGCCATGGGCCACCGCTGCACGC	281	
Db	1376	GGAGGGAGGTGCGATTGTTGTATCGATCG	CGCTGTGTACGCCATGGGCCACCGCTGCACGC	1435	
Qy	282	CATGACCGTGCACCTGTGTCGCGCGGTAG	AGACTCTGCGCTCGCATGAGACCCCGTGA	341	
Db	1436	CATGACCGTGCACCTGTGTCGCGCGGTG	GGGCTCTGCGCGCATGAGACCTCTGTAGA	1495	
Qy	342	TGGCACCCAGCTGCTTAAGTACATCAG	AAAGCTCAACTTCTCAGGCAATTCGCGGGAACCC	401	
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Qy	402	TGTAACTTCAATGAGAACGGAGACGCA	CCGGGGCGCTACGACATCTTACCAGTACCAACT	461	
Db	1556	TGTGACCTTCAATGAGAATGGAGATG	CGCTGTGGCGCTATGACATCTTACCAATACAGCT	1615	
Qy	462	GCGCAATGGCTCGGCGGAGTACAAGGT	CATCGGCTCGTGGACAGACCACTGCACTCAG	521	
Db	1616	GCGCAACGATTTCTGCCGAGTACAAG	GTCATTTGGTCTCTGGACTGACCACTGCACTTAG	1675	
Qy	522	AATAGAGCGGATGACAGTGGCCAGGAG	TGGCAGCAGCTCGCGGCTCCATCTGCGAGCT	581	
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Qy	582	GCCCTGCCAGCCCGGGAGCGAAAGAG	ACTGTGAAGGGCATGGCTGTGCTGGCACCTG	641	
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Qy	702	CGACATGGCGCCACAGAGAACCGCAG	AGCTGCCAGCCCATCCCATCTGTCAGTTGGA	761	
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Db	1976	GTTGTTGCTGTGTGTGTGTGTGTGTG	TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2035	
Qy	882	CGGGGACTGAGCTACGCTGCTGCTG	CGCGGCATCTTCTGTGTGTGTGTGTGTGTGT	941	
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Qy	942	CATGATCGCAGACCGGACCTTGGGG	ACCTGTTGCTCCGCGCATCTTCTTAGGGCTCG	1001	
Db	2096	CATGATCGTGTGAGCCCGACCTTGG	CACTGCTCGCGCGCATCTTCTTAGGGCTCG	2155	
Qy	1002	CATGAGCATCAGCTACGCGCGCTGTG	ACAAAGCAACCGCATTTACCGATCTTGA	1061	
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QY 1062 GCAGGCAAAACGGTCAGTCCAGTCCCGCGTTTTCATCAGCCCGCGCTCGCAGCTGGCCAT 1121
Db 2216 GCAGGGCAAGCGCTCGTTCAGTGGCCCGCGCTTCATCAGCCCGCGCTCACAGCTGGCCAT 2275
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QY 1182 CTCCTCATCTGGTGGTGGATCTCCAGGACCAACCGGACACTTGGACCCCGCTTTGCCAGGG 1241
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Db 2456 GCTCATGTGTACGTGTACTGTGTAGCCATCAAGACCCGAGCGGTGCGGAGACCTTCAA 2515
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DEFINITION Sequence 175 from Patent WO02061087.
ACCESSION AX548890
VERSION AX548890.1 GI:25813754
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 175 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
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ORIGIN

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Query Match 83.8%; Score 1470.8; DB 6; Length 3884;
Best Local Similarity 91.1%; Pred. No. 1.9e-233; Indels 0; Gaps 0;
Matches 1562; Conservative 0; Mismatches 152;

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Db 1256 TGCCGAGTTCTGGAGAGCAACTTTCATTTGCAATTGAGCGGCCACCGGGTCAAGAGGG 1315
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QY 222 GGAGGGGAAGGTGAGTTCGTTGATTCGCTGTGTAGCGCATGGGCCACCGCGCTGCAGCG 281
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